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Gaps
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02-MAR-2004 (TrEMBirel. 27, Last sequence update)
02-MAR-2004 (TrEMBirel. 27, Last annotation update)
02-MAR-2004 (TrEMBirel. 27, Last annotation update)
03-MAR-2004 (TrEMBirel. 27, Last annotation update)
Microtubule aggregate protein (Fragment).
Pagrus major (Red sea bream) (Chrysophrys major).
Bukaryota, Metazoa, Chordate, Craniara, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen S.L., Xu M.Y.,
"Analysis of expressed genes in red sea bream (Chrysophrys major).",
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY190714, AAP20189.1;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Branchioscoma floridae (Florida lancelet) (Amphioxus).
Eukaryota, Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.7%; Score 60; DB 2; Length 110; Best Local Similarity 59.1%; Pred. No. 1.3; Matches 13; Conservative 3; Mismatches 6; Indels
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SEQUENCE FROM N.A.
MEDLINE=21980198; PubMed=11967531;
Abi-Rached L., Gilles A., Shiina T., Fontarotti P., Inoko
Abi-Rached E., Gilles A., Shiina T., Fontarotti P., Inoko
"Evidence of en bloc duplication in vertebrate genomes.";
"Fyidence of en bloc duplication in vertebrate genomes.";
     Indels
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EMBL. AF91295; AAM18895.1; -.
Hypothetical protein.
SEQUENCE 651 AA; 73083 WW; 589DC917FAC000A6 CRC64;
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ف
                                                                                                                                                                                                                  110 AA.
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  Mismatches
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                                                                                           89 DSLILSALRAMIDFGDDFINKI 110
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                                                6 DVLILSALRRMLWAADDFLEDL 27
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Best Local Similarity 57.1:
...Ahes 12; Conservative
13; Conservative
                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparidae, Pagrus.
NCBI_TaxID=143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                  AAP20189
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Q8T749
  Matches
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O6NM08
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Microtubule aggregate protein (Fragment).
Pagrus major (Red sea bream) (Chrysophrys major)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Percoidei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRNIN-BALB/C x BALB.B F1; TISSUE-ConA-activated spleen cells;
STRNIN-BALB/C x BALB.B F1; TISSUE-ConA-activated spleen cells;
MEDLINE-20471514; PubMed-11021531;
Malarkannan S., Horng T., Eden P., Gonzalez P., Shih P.,
Brouwenstijn N., Klinge H., Christianson G., Roopenian D., Shastri l'abfferences that matter: major cytotoxic T cell-stimulating minor histocompatibility antigens.";
Immunity 13:333-344 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBL_TaxID=10090;
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STRAIN-BALB/c x BALB.B F1; TISSUE-CONA-activated spleen cells; Malarkannan S., Shastri N.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 2; Length 449; 9.1e-06;
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Pred. No. 1.3;
Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY190714; AAP20189.1; -.
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MGD, MGI:95975; H28.
QG), GO:0006955; P:immune response; IDA.
SEQUENCE 449 AA, 50059 MW; 3010B42ACA7490AD CRC64;
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                                                                                                                                                                                                                                                        01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
     4
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                                                                         392 LDPVKDMLILSALKEILYTANEFLEDLPLNK 422
                                                                                                                                                                                                                  449 AA.
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                                             1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQ 31
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60.6%; Pred. No. 9.1e
:ive 6; Mismatches
7; Mismatches
                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                   Minor histocompatibility antigen
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59.1%;
20; Conservative
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                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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les 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                          Name=H28
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099DB7
AC 099DB8
AC 099DBB
DT 01-JU
DT 01-JU
DT 01-CC
DE WARN
CC NAME M
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CO N
Matches
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29-MAR.2004 (TrEMBLrel. 27, Last sequence update)
29-MAR.2004 (TrEMBLrel. 27, Last sequence update)
41-39-2004 (TrEMBLrel. 27, Last annotation update)
41-39-2009:
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
NCBI_TaxID=3702;
                                            GENMUS;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
At3932092.
At39dopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mangnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim C.J., Chen H., Cheuk R., Shinn P., Carninci P., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Narusaka M., Sakurai T., Satou M., Saki M., Shinozaki K., Ecker J.R., Seki M., Shinozaki K., Ecker J.R., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BT012169; AAS76264.1; -.
Interpro, IPR005162; Retrotrans gag.
Pfam; PP03732; Retrotrans gag.
SEQUENCE 190 AA; 21466 WW; 821E390B7C17A67B CRC64;
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Kim C.J., Chen H., Cheuk R., Shinn P., Carninci P., Hayashizaki Y.,
Ishida J., Kamiya A., Kawai J., Narusaka M., Sakurai T., Satou M.,
Saki M., Shinozaki K., Ecker J.R.;
"Arabidopsis ORF clones.";
"Arabidopsis ORF clones.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL: BT012169; AAS7626411; -.
SEQUENCE 190 AA, 21466 MW; 821E390B7C17A67B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 56; DB 2; Length 190; 37.0%; Pred. No. 9; tive 8; Mismatches 9; Indels
190 AA.
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     PRT;
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Matches 10; Conservative
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Matches 10; Conservative
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PRELIMINARY;
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           Q6NM08
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AAS76264
ID AAS76
AC AAS76
DT 29-MP
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Search completed: November 10, 2004, 13:38:22 Job time: 43.2953 secs

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US-08-249-383-3
US-08-249-983-3
Patent No. 5646011
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US-08-461-361-183

US-08-485-910-183

PCT-US-06-266-157

US-09-28-352-4674

US-09-248-7964-15595

US-09-248-7964-15595

US-09-248-7964-14837

US-09-262-991A-31716

US-09-560-236-31759

US-09-560-236-31759

US-09-170-496D-104

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 29; Conserv
     RESULT 1
US-08-224-983-2
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US-08-852-933-2
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Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 41860, A
Sequence 41860, A
Sequence 20, Appl
Sequence 4120, Appl
Sequence 4123, Appl
Sequence 4124, A
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 115, Appl
Sequence 15, Appl
Sequence 115, Appl
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183, App
183, App
183, App
                                                                                                                          November 10, 2004, 12:32:37; Search time 10.7081 Seconds (without alignments) 191.991 Million cell updates/sec
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Sequence
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1: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/ptTUS_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/ptTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-224-983-2
US-08-852-945-2
US-08-853-021-2
US-08-853-021-2
US-09-098-079-13
US-09-098-079-13
US-09-270-767-44872
US-09-270-767-44872
US-09-270-767-44872
US-09-270-767-44872
US-09-270-767-44320
US-09-270-767-14238
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US-09-270-767-1654
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US-09-270-767-1654
US-09-270-767-1654
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US-09-248-7968-25835
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US-09-248-7968-25835
US-09-238-328-1283
US-08-415-183
US-09-328-328-1283
US-08-415-183
US-08-415-183
US-08-415-183
US-08-415-183
US-08-415-183
US-08-415-183
US-08-415-183
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148
1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Gaps

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Gaps

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NESOLO-853-021-2
; Sequence 2, Application US/08853021
; Sequence 2, Application US/08853021
; Parent No. 8588700
; GENERAL INFORMATION:
; TILLE OF INVENTION: Cisplatin Resistance Gene and Uses Therefor
; VUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                              Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.5%; Score 134; DB 2; Length 83; Best Local Similarity 93.5%; Pred. No. 2.6e-13; Matches 29; Conservative 1; Mismatches 1; Indels
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Pred. No. 2.6e-13;
1; Mismatches 1;
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION NUMBER: US/08/853,021
FLING DATE: 08-MAY-1997
CLASSIFICATION: 435
PRIOR PAPLICATION NUMBER: 08/24,983
FLING DATE: 08-RAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: GIULIO A. DECORT, UF.
REGISTRATION NUMBER: BBI-010
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: CARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,983
FILING DATE: 08-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 01.110 A. DECORT, Jr.
REGISTRATION NUMBER: 31,503
REFRENCE/DOCKET NUMBER: 31,503
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION POR SEQ ID NO: 2:
ENGURNIC FIRACTERISTICS:
LENGTH: 83 amino acids:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.5%;
Matches 29; Conservative 1
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LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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TYPE: am
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Sequence 2, Application US/08852933
Patent No. 5846725
GENERAL INFORMATION:
APPLICANT: VOKOyama, Shiro
TITLE OF INVENTION: Cisplatin Resistance Gene and Uses Therefor NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08852945
; Patent No. 5858674
; GENERAL INFORMATION:
APPLICANT: Yokoyama, Shiro
TITLE OF INVENTION: Cisplatin Resistance Gene and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.5%; Score 134; DB 2; Length 83; Best Local Similarity 93.5%; Pred. No. 2.6e-13; Matches 29; Conservative 1; Mismatches 1; Indels
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/852,945
FILING DATE: 08-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,933
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/224,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNAY AGANT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REPRENCE/DOCKET WINNBER: BBI-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPRAX: (617)227-5941
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   ZIP: 02109-1875
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SWOTHWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-852-933-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
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Gaps

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Sequence 13, Application US/09098079

Sequence No. 6489095

GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corrina
APPLICANT: Glosh, Soumitra S.

APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Davis, Robert E.

TITLE OF INVENTION: EXTRAMITOCHONDBRIAL DNA
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS: 26

CORRESPONDENCE ADDRESS: 26

CORRESPONDENCE ADDRESS: 4

STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: USA

STATE: Washington

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-UM-1998
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
REGISTRATION WHBER: 43,058
REGISTRATION NUMBER: 43,058
REGISTRATION NUMBER: 43,058
REGISTRATION NUMBER: 43,058
REGISTRATION NUMBER: 660088,416
TELEGRAM: (206) 622-4900
TELEGRAM: (206) 622-4900
TELEGRAM: (206) 622-4900
TELEGRAM: COSO 682-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                             CALP: 98104

CAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION NOWBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION NOWBER: G60088.417
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMULICATION INFORMATION:
TELEPHAN: (206) 622-4900
TELEPHAN: (206) 622-4900
TELEPAX: (206) 622-6031
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ANLLLIVPILIAMAFLMLTERKILGYMQLR 34
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US-09-097-889-13
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-098-079-13
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RESULT 6

REQUENCE 2, Application US/08852865

Sequence 2, Application US/08852865

Sequence 2, Application US/08852865

Recent No. 6046044

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICANT: Yokoyama, Shiro

TITLE OF INVENTION:

CORRESPONDENCE: 4 COCKFIELD

STREET: 60 State Street, suite 510

STREET: 60 State Street, suite 510

STREET: 60 State Street, suite 510

STREET: 80 Ston

STREET: 60 State Street, suite 510

STREET: 80 Ston

TELECOMMUNICATION INPERRATION:

TOTAL STREET: 80 STON

TOTAL STREET: 80 STON

TELECOMMUNICATION INPERRATION

TOTAL STREET: 80 STON

TELECOMMUNICATION INPERRATION

TOTAL STREET: 80 STON

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TELECOMMUNICATION

TOTAL STREET: 80 STON

TOTAL STREET: 80 STON
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Patent No. 618117

GENERAL INFORMATION

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Davis, Robert E.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING

TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RS, NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.5%; Score 134; DB 3; Length 83; 93.5%; Pred. No. 2.6e-13; tive 1; Mismatches 1; Indels
1 ANLLLLMVPILIAMAFLMLTERKILGYIOPR 31
                                  2 ANLLLLIVPILIAMAFLMLTERKILGYIQLR 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.5
Best Local Similarity 93.5
Matches 29; Conservative
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CITY: Se
STATE: P
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Gaps

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RESULT 10
US-09-248-796A-14320
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US-08-928-692-20
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APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 3226-094
CURRENT PAPLICANTION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41860
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-02-270-767-44872
Sequence 44872, Application US/09270767
Sequence 44872, Application US/09270767
Sequence 44872, Application US/09270767
Septembly Conservation:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT PELING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 44872
LENGTH: 286
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                         Query Match 88.5%; Score 131; DB 4; Length 318; Best Local Similarity 90.3%; Pred. No. 3.4e-12; Matches 28; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.1%; Score 83; DB 4; Length 286
Best Local Similarity 57.1%; Pred. No. 6.7e-05;
Matches 16; Conservative 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.8%; Score 87; DB 4; I
llarity 60.7%; Pred. No. 1.8e-05;
Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                       4 ANLLLLIVPILIAMAFLMLTERKILGYMQLR 34
                                                                                                                                                                                                             1 ANLLLLMVPILLAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-44872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:::||::||| |||||| ||||1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LLLMVPILIAMAFLMLTERKILGYIQPR 31
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                                                                                                                                                                                                                                                                                                                                                      Sequence 41860, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Drosophila melanogaster
    LENGTH: 318 amino acids
                      TYPE: amino acid STRANDEDNESS:
                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
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US-09-098-079-13
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Sequence 19420, Application US/03248796A
PREACT 19420, Application US/03248796A
GORRAL PROBANION:
GORRAL PROCESSION OF 60.713
APPLICATION FAITH PROBADION:
TITLES OF INVESTION TO CANDIDA ALBICOME
TITLES OF INVESTION OF 1220-102-13
FRICKS PRINCE TOTAL OF 1220-13
FRICKS PR
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1 ANLLLLMVPILIAMAFLMLTERK 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-270-767-56454
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US-09-583-110-4394
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APPLICANT: Yaver, Deborah S.
APPLICANT: Yaver, Deborah S.
APPLICANT: Ames, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.
                                                                             Gaps
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                                     DB 2; Length 371;
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                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
CURFORMARE: FastSEQ for Windows Version 2.0
CURFORT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
                                     42.6%; Score 63; DB 2
41.4%; Pred. No. 0.1;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%; Score 63; DB
41.4%; Pred. No. 0.1;
tive 10; Mismatches
                                                                                                                   3 LLLLMVPILLAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LLLLMVPILIAMAFLMLTERKILGYIQPR 31
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                                                                                                                                          : | | :: | | | : | : : | | | : : | | | 13 VLLVLVPSLLAVAYVTVAERKTMASMQRR
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US-09-270-767-41238
; Sequence 41238, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION;
; APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/ABENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                    Sequence 20, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: No. 6323002e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 371 amino acids
amino acid
                                 Query Match
Best Local Similarity 41.4%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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US-09-339-972-20
US-08-928-692-20
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Sequence 56454, Application US/09270767

Parent No. 6703491

GRNERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: ParentIn Ver. 2.0

SEQ ID NO 56454

LENGTH: 189
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTARRE: Patentin Ver. 2.0
SEQ ID NO 41238
LENGTH: 189
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                   Query Match
35.8%; Score 53; DB 4;
Best Local Similarity 43.5%; Pred. No. 1.6;
Matches 10; Conservative 8; Mismatches 5
                                                                                                                                                                                FEATURE:
, OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-56454
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, ORGANISM: Streptococcus pneumoniae US-09-583-110-4394

0; Gaps Query Match 35.1%; Score 52; DB 4; Length 850; Best Local Similarity 33.3%; Pred. No. 13; Matches 8; Conservative 10; Mismatches 6; Indels

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Search completed: November 10, 2004, 13:44:01 Job time : 11.7081 secs

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14
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                                                                                                                                                                                                                                   November 10, 2004, 16:36:12; Search time 33.3022 Seconds (without alignments) 328.807 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/DSO6_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
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11: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
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18: /cgn2_6/prodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/prodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                US-10-092-750-26
148
1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 26, Appl Sequence 13, Appl Sequence 14, Appl Sequence 189, Appl Sequence 3171, Ap Sequence 310657, Sequence 2416, Ap Sequence 226150, Sequence 27815, Ap Sequence 226150, Sequence 226150, Sequence 226150, Sequence 226150, Sequence 270, Appl Sequence 20, Appl Description 4 US-10-092-750-26 US-09-098-079-13 5 US-10-428-487-34 6 US-10-428-487-34 6 US-10-464-049-3171 7 US-10-425-115-310657 6 US-10-428-487-55 5 US-10-264-049-3416 5 US-10-424-599-226150 5 US-10-424-599-226150 7 US-10-428-115-332406 7 US-10-425-115-202752 Query Match Length DB 31 318 318 318 3218 318 318 348 134 148 1131 1131 1130 1120 11 120 664 664 Score No. Result

RESULT 2
US-09-079-13
'Sequence 13, Application US/09098079
'Patent No. US20020064773A1
'GENERAL INFORMATION:

	ength 31; ndels 0; Gaps 0;
US-10-424-599-161174 US-10-282-1224-45946 US-10-281-1224-45995 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-781-014-654 US-10-48-625-2 US-10-48-625-2 US-10-48-68-421 US-10-626-623-35-9 US-10-628-72-191 US-10-628-72-191 US-10-628-72-191 US-10-628-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-688-72-191 US-10-70-70-70-70-70-70-70-70-70-70-70-70-70	Score 148; DB 14; L Pred. No. 3.3e-14;  ); Mismatches 0; I TERKILGYIQPR 31
60 40.5 138 555 37.2 261 555 37.2 261 552 35.1 204 552 35.1 204 552 35.1 204 552 35.1 204 552 35.1 204 552 35.1 204 552 35.1 584 552 35.1 584 650 33.8 513 851 851 850 33.8 513 851 850 33.8 513 850 33.8 513 850 33.8 513 850 33.8 513 850 33.8 513 850 33.8 513 850 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 33.1 106 49 49 49 33.1 106 49 49 49 33.1 106 49 49 49 33.1 106 49 49 49 33.1 106 49 49 49 33.1 106 49 49 49 33.1 106 49 49 49 49 33.1 106 49 49 49 49 49 49 49 49 49 49 49 49 49	tch al Similarity 100. 31; Conservative 1 ANLLLLAVPILIAMAE 1 ANLLLLAVPILIAMAE 1 ANLLLLAVPILIAMAE
14 11 11 11 11 11 11 11 11 11 11 11 11 1	Query Mat Best Loca Matches Qy Db

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Gaps

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NAME/KEY: MISC_FEATURE LOCATION: (1) OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (3) - OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JAPPLICANT: Glosh, Sounitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Pahy, Eoin D.
APPLICANT: Taylor, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glosn, Gary M.
APPLICANT: Glosn, Gary M.
APPLICANT: GIBEN, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TRAGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10 DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10 DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 3003-04-04
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 189
LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3171, Application US/10264049

Publication No. US20040005579A1

GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION:
NUCLERET APPLICATION Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.5%; Score 131; DB 16; Length 318; 90.3%; Pred. No. 1.2e-10;
                                                                                                                                       Indels
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                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 189, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                           7
                                                                                                                                       28; Conservative
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US-10-408-765A-189
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                           Matches
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APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Pany, Boin F.
ITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
ITTLE OF INVENTION: EXTRAMITOCHONDERAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and TOTALED TOTAL
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| Sequence 34, Application US/10428487
| Sequence 34, Application US/10428487
| Subjication No. US20040006780A1
| GENERAL INFORMATION
| APPLICANT: RASTELL! LUCA K.
| APPLICANT: GENER, HANS-PETER
| TITLE OF INVENTION: VEGF-MODILATED GENES AND METHODS EMPLOYING THEM
| TITLE OF INVENTION: VEGF-MODILATED GENES AND METHODS EMPLOYING THEM
| TITLE OF INVENTION: VEGF-MODILATED GENES AND METHODS EMPLOYING THEM
| TILL REPERENCE: 09800080-0103
| CURRENT PELING DATE: 2003-05-02
| PRIOR APPLICATION NUMBER: 09/815,153
| PRIOR PILING DATE: 2000-03-22
| NUMBER OF SEQ ID NOS: 84
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.5%; Score 131; DB 9; Length 318; 90.3%; Pred. No. 1.2e-10; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION ATSPORMENTAN.
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Pred. No. 1.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,088 .416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.5%;
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nes 28; Conservative
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CORGANISM: Homo sapiens
US-10-428-487-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
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Best Local Similarity
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US-09-098-079-13
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Matches
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Sequence 226150, Application US/10424599
| Sequence 226150, Application US/10424599|
| Sequence 226150, Application US/10424599|
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua |
| APPLICANT: Cao Yongwei |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Dia Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Dia Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Dia Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Dia Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Dia Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION NUMBER: US/10/424.599 |
| CURRENT APPLICATION NUMBER: US/10/424.599 |
| VUMBER OF SEQ ID NOS: 285684 |
| SEQ ID NO 226550 |
| LENGTH: 110
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US-10-264 049-3416

Sublication No. US20040005579A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT PELIAG DATE: 2002-10-04

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR APPLICATION NUMBER: US 60/209,467

NUMBER OF SEQ ID NOS: 4360

SEQ ID NO 3416

LENGTH: 79
                                                                                                                                                                           Score 127; DB 16; Length 318;
Pred. No. 4.5e-10;
2; Mismatches 1; Indels (
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US-10-424-599-226150
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ORGANISM: Glycine max
FRATURE:
NAME.(X. unsure
LOCATION: (1)..(110)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.9%; Pred. No. 1e-(
Matches 26; Conservative 1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1490
LENGTH: 318
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Best Local Similarity 90.0%;
Matches 27; Conservative 2
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ORGANISM: Homo sapiens
                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1490
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     FEATURE:
MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                        ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-3171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 310657, Application US/10425115

Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Experience Toou, Yihua

APPLICANT: Cao, Yonwa

APPLICANT: Cao, Yonwa

APPLICANT: APPLICANT: Usous Sequence Title Of Invention: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: 2003-04-28

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 310657

LENGTH: 261
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; Sequence 1490, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Tahy, Each D.
; APPLICANT: Taylor, Bradford W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TILLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3073
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                                                                                                                                                                                                                                                              Length 101;
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.3%; Pred. No. 4.8e-11;
Matches 28; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: MRT4577_46377C.1.pep
US-10-425-115-310657
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ilarity 93.3%; Pred. No. 1.3e-10;
Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(261)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLLLLIVPILIAMAFLMLTERKILGYIQLR 30
                                                                                                                                                                                                                                                                                                                                                              2 NLLLLMVPILIAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                                            21 NLLLLIVPILIAMAFLMLTERKILGYIQLR 50
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                                                                                                        FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
....hes 28; Conservat
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US-10-408-765A-1490
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TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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LENGTH: 46
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US-10-000-845-20
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APPLICANT: And H.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms of TITLE OF INVENTION Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA. 034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/260,308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/260,308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/260,308
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR APPLICATION NUMBER: 60/260,308
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR P
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                                                                                           Gaps
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                                                                                       1,
            DB 15; Length 110;
                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
    Score 111.5; DB 19
Pred. No. 2.5e-08;
2; Mismatches 2
                                                                                                                                                                  1 ANLLLLMVPILLAMAFLML-TERKILGYIQPR 31
                                                                                                                                                                                                               17 APLLLLIVPILIAIAFLMLXTERKILGYIQLR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.9%; Score 65; DB Best Local Similarity 41.4%; Pred. No. 0.46 Matches 12; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LLLLMVPILIAMAFLMLTERKILGYIQPR 31
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28 ILVVSVVILLCVAYLILWERKLIGWMHVR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47875, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Aamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Burkholderia cepacia
US-10-282-122A-47875
Query Match
Best Local Similarity 84.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-425-115-332406
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; Sequence 332406, Application US/10425115 ; Publication No. US20040214272A1

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Uncleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION WUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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0
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TITLE OF INVENTION: Methods for Modifying the Production of
a Polypeptide
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.2%; Score 64; DB 17; Length 46; 82.4%; Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc. STRET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER IS CALL.

COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE TASTERO, FOR Windows Version 2.0
SOFTWARE: FastERO, for Windows Version 2.0
CLASSIFICATION NUMBER: US/10/000,845
FILING DATE: 24-Oct-2001
CLASSIFICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Flias J
RECISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION NUMBER: 4944.200-US
                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: unsure

; LOCATION: (1)...(46)

; OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_6626C.1.pep

US-10-425-115-332406
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Publication No. US20040197854A1
GENERAL INFORMATION:
APPLICANT: Ercdy, Howard
YAVEY, Deborah S.
Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AMAFLMLTERKILGYIQ 29
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ZIP: 10174
COMPUTER READABLE FORM:
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Best Local Similarity 82.4$
Matches 14; Conservative
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFREENCE: ELITAA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/194,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-23

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-12-2

PRIOR APPLICATION NUMBER: 60/25,655

PRIOR PLING DATE: 2000-12-2

PRIOR APPLICATION NUMBER: 60/25,655

PRIOR PLING DATE: 2000-12-2

PRIOR APPLICATION NUMBER: 60/25,636

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/26,636

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/26,636

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-17

PRIOR PLING DATE: 2001-02-17
                                                                                                                                                                                                                  Length 138;
                                                                                                                                                                                                                                                                                    9; Indels
                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_116558C.1.pep
US-10-424-599-161174
                                                                                                                                                                                                              Query Match
40.5%; Score 60; DB 15;
Best Local Similarity 37.9%; Pred. No. 0.86;
Matches 11; Conservative 9; Mismatches 9.
           LOCATION: (1)..(138)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                          3 LLLLMVPILLAMAFLMLTERKILGYIQPR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45946, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (66)..(66)
OTHER INFORMATION: X=any
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 161174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 202752, Application US/10425115

publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cavalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cavalic, David K.

APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Number: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 202752

LENGTH 134
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                                                                                                                                                                                                                                                   Query Match 42.6%; Score 63; DB 17; Length 371; Best Local Similarity 41.4%; Pred. No. 0.93; Matches 12; Conservative 10; Mismatches 7; Indels
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; OTHER INFORMATION: Clone ID: MRT4577_11649C.1.pep
US-10-425-115-202752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(134)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                            3 LLLLMVPILIAMAFLMLTERKILGYIQPR 31
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-000-845-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
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LOCATION: (1)..(
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US-10-424-599-161174
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Search completed: November 11, 2004, 01:28:08 Job time: 34.3522 secs

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us-10-092-750-40.rai

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November 10, 2004, 12:32:37; Search time 6.90846 Seconds (without alignments) 191.991 Million cell updates/sec
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1: /cgT2 6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgT2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgT2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgT2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgT2 6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgT2 6/ptodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   using sw model
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Gapop 10.0 , Gapext 0.5
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106
1 SSQALRIHQWIHLFSDFTST
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Maximum DB seq length: 2000000000
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Sequence 18650, A Sequence 4877, Ap Sequence 1806, A Sequence 18249, A Sequence 24016, A Sequence 6, Appliseduence 23331, A Sequence 6, Appliseduence 6, Applis
                                                                                                                     Description
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Sequence
Sequence
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                                                                                                                                                                                  US-09-248-796A-18650
US-09-328-322-4877
US-09-221-976-5966
US-09-252-991A-18086
US-09-278-796A-1849
US-09-270-767-4272
US-09-270-767-4272
US-09-270-767-2273
US-09-270-767-2273
US-09-248-796A-23739
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US-09-248-796A-23739
US-09-248-796A-23739
US-09-1248-796A-23739
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US-09-134-002-6
US-08-392-210-6
US-08-392-210-6
US-08-464-052-2
US-08-464-052-2
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US-08-464-052-2
US-08-464-052-2
US-08-464-052-2
US-08-464-052-2
US-08-68-411-2
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SUMMARIES
                                                                                                                     Length DB
                                                                              Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                    40.5
40.5
40.5
70.5
                                                                                                                     Score
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Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	
US-08-468-852-6	US-08-468-857-6	US-09-248-796A-27358	US-09-270-767-33889	US-09-270-767-49106	US-08-414-926A-23	US-08-926-922-23	US-09-253-682-23	US-09-527-657-23	US-09-892-100-23	US-09-252-991A-16816	US-09-489-039A-10279	US-09-248-796A-27519	US-09-107-532A-4388	US-09-270-767-35656	US-09-270-767-50873	US-09-270-767-45599	US-09-903-456-37	
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330	330	65	153	153	214	214	214	214	214	222	585	87	770	108	108	224	276	
38.2	38.2	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.3	37.3	36.8	36.8	36.8	36.8	
40.5	40.5	40	40	40	40	40	40	40	40	40	40	39.5	39.5	on M	ტ ლ	ี ค	8	
28	29	30	31	32	33	34	. E	36	3.7	00	66	40	41	42	43	44	45	

## ALIGNMENTS

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Sequence 18650, Application US/09248796A

Fatent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOULD AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WOUNDER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 28208

SEQ ID NO 18650
LENGTH: 156
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US-09-328-352-4877
US-09-328-352-4877
Sequence 4877, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4877
LENGTH: 1005
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Best Local Similarity 52.6%; Pred. No. 1.3;
Matches 10; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; CRGANISM: Acinetobacter baumannii
US-09-328-352-4877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSQALRIHQWLHLFSDFTS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 SFQPVTIHTSLHIFKNFTS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-248-796A-18650
US-09-248-796A-18650
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DB 4; Length 1005;

43.4%; Score 46;

Query Match

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APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG FILE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS PLLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: 05/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR PILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NOS: 28208 LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-222-991A-24016

Sequence 24016, Application US/09252991A

Sequence 24016, Application US/09252991A

Sequence 24016, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24016
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Sequence 42272, Application US/09270767

Sequence 42272, Application US/09270767

Patent No. 6703431

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

CURRENT PAPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.6%;
                                                                                                                                                                                                                                                                                                                                                                        Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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71 HEWVHLYDD 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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Matches 7; Conserv
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LENGTH: 402
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Sequence 18086, Application US/0925291A
Sequence 18086, Application US/09252991A
Sequence 18086, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGATMOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABENGATMOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABENGATMOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18086
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                                 4; Indels
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                                                                                                                                                                                                                                                    Sequence 5966, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERSONS: GENERAL US/09/621,976
CURRENT FILING DATE: 2000-07-21
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 5966
     Best Local Similarity 53.8%; Pred. No. 42; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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; Patent No. 6747137
; GENERAL INFORMATION:
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US-09-252-991A-18086
                                                                                                                2 SOALRIHOWLHLF 14
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Best Local Similarity 41.77
Matches 10; Conservative
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Matches 8; Conservative
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.US-09-621-976-5966
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Ouery Match 39.6%; Score 42; DB 4; 18est Local Similarity 46.7%; Pred. No. 1.1e+02; Matches 7; Conservative 4; Mismatches 4
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DOCATION: (B) LOCATION 1...594

SEQUENCE DESCRIPTION: SEQ ID NO: 6929:

US-09-107-532A-6929
                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
REGISTRATION NUMBER: 40,489
REFERENCE DOCKET NUMBER: GTC
TELECOMUNICATION INFORMATION:
TELEPAX: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6929:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 amino acids
TYPE: amino acid
    40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 KIHKYFHEFSNFLPT 23
                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity 58.3
7, Conservative
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: BUTEROCCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                           Query Match
40.6%; Score 43; DB 4; Length 402;
Best Local Similarity 56.2%; Pred. No. 48;
Matches 9; Conservative 3; Mismatches 4; Indels
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65;
                                                                                                                                                                                                                                                                         Sequence 8, Application US/09293549
; Sequence 8, Application US/09293549
; Patent No. 6440409
; GENERAL INFORMATION:
    APPLICANT: G. Todd Milne
; APPLICANT: G. Todd Milne
; TITLE OF INVENTION: A METHOD FOR EFFICIENT AND HIGHLY
; TITLE OF INVENTION: A METHOD FOR EFFICIENT AND HIGHLY
; TITLE OF INVENTION: SELECTIVE CONTROL OF MICROORGANISMS
; FILE REFERENCE: 50078/008002
; CURRENT FILING DATE: 1999-04-16
; EARLIER FILING DATE: 1999-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.6%; Score 43; DB
Best Local Similarity 50.0%; Pred. No. 65;
Matches 10; Conservative 2; Mismatches
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-293-549-8
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COUNTRY: USA
                                                                                                                                                                     271 SLIHLSKHLFANFTS 286
                                                                                                                                      4 ALRIHOWLHLFSDFTS 19
  US-09-270-767-42272
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Sequence 23739, Application US/09248796A

Patent No. 6747137

Batent No. 6747130:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 23739

LENGTH: 63
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US-09-248-796A-23391
5 Sequence 23391, Application US/09248796A
5 Sequence 23391, Application US/09248796A
5 Patent No. 6747137
6 GENERAL INFORMATION:
7 ITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
7 ITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
7 ITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
7 ITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
7 ITLE OF INVENTION: NUMBER: US/09/248,796A
7 CURRENT APPLICATION NUMBER: US/09/248,796A
7 CURRENT FILING DATE: 1999-02-12
7 PRIOR FILING DATE: 1998-02-13
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Length 594;
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Pred. No. 14;
Nismatches 4, Indels
                                                    4; Indels
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US-08-461-002-6
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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Upake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
ZIP: 14603
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                   ;
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) Sequence 4944, Application US/09513999C

) Patent No. 6783961

| Patent No. 678361

| Patent No. 678361

| APPLICANT: Dumas Milne Edwards, J.B.

| APPLICANT: Dumas Milne Edwards, J.Y.

| APPLICANT: Duclert, A. J.Y.

| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

| PAPLICANT: Glordano, J.Y.

| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

| PRICANT: BAPLICATION NUMBER: US/09/513,999C

| CURRENT APPLICATION NUMBER: US 60/122,487

| PRIOR PILING DATE: 1999-02-26

| NUMBER OF EXQ ID NOS: 36681

| SEQ ID NO 4944

| LENGTH: 115

| LENGTH: 115
                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 26;
                                                                                                                                                                                                              Query Match 38.7%; Score 41; DB 4; Length 93; Best Local Similarity 53.3%; Pred. No. 21; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23391
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa=Pro or Thr
US-09-513-999C-4944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ASRIMNLYQFIQLYKDITS 112
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US-08-464-052-6
'Sequence 6, Application US/08464052
'Patent No. 6008201
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Best Local Similarity 31.6%;
Matches 6; Conservative E
                                                                                                                                                                                                                                                                                                                5 LRIHQWLHLFSDFTS 19
                                                                                                                                                                                                                                                                                                                                                           LNVHOEFLVFSNFTS 87
                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   US-09-248-796A-23391
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Sequence 6, Application US/08461002
Patent No. 6214543
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
COUNTRY: U.S.A.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Goldman, Micheel L.
REGISTRATION NUMBER: 19603/185 (D-1485B)
TELEFORMULICATION INFORMATION:
TELEFORMULICATION INFORMATION:
TELEFORMULICATION INFORMATION:
TELEFORM: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acide
TYPE: amino acide
TYPE: Amino acide
TYPE: Amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19603/186 (D-1485B)
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Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603
TELECOMMUNICATION: INFORMATION:
"TELECOMMUNICATION: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: TWO THE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ALRIHOWLHLFSDFTST 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 AQRVMDWLHPDGDLTDT 45
                                                                                                                                                                                                                                                                                                                                                                                              / MOLECULE TYPE: peptide
US-08-464-052-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
; TOPDLOGY: unknown
; MOLECULE TYPE: peptide
US-08-461-002-6
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OW 4 ALALINOWHILESDEPST 20

THE SOURCE ADDICATED 45

RESULT 15

US-08-689411-6

SQUENCE 6. Application US/08689411

FARENCE NO. 6228981

FARENCE NO. 6228981

FARENCE CONSTRUCTION CONDUCTOR PREACHENING FOR WICCORNING FOR WICCORNING TO WINDSTRUCTION CONDUCTOR THEREOF WINDSTRUCTION CONDUCTOR THEREOF WINDSTRUCTION CONDUCTOR THEREOF WINDSTRUCTION CONDUCTOR THEREOF CONDUCTOR THE PROPERTY OF STATEM FOR THE PROPERTY OF ST
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Db 29 AQRVMDWLHPDGDLTDT 45
Search completed: November 10, 2004, 13:44:10
Job time : 6.90846 secs

4 ALRIHOWLHLFSDFTST 20

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us-10-092-750-40.rapb

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RESULT 2
US-10-425-115-317501
; Sequence 317501, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INPORMATION:
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Sequence 42, Appl
Sequence 704, Appl
Sequence 704, Appl
Sequence 3185, Ap
Sequence 9, Appli
Sequence 7011, A
Sequence 7011, A
Sequence 7011, A
Sequence 3855, A
Sequence 35561,
Sequence 25553,
Sequence 25553,
                                                                                    November 10, 2004, 16:36:12; Search time 21.4853 Seconds (without alignments) 328.807 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

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2: /cgm2_6/ptodata/1/pubpaa/PCT_NBW_PUB.pep:*
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13: /cgm2_6/ptodata/1/pubpaa/US09_NBW_PUB.pep:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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7 US-10-425-115-317501
8 US-10-302-267-42
5 US-10-412-699B-704
4 US-10-4047-2357
7 US-10-425-115-341865
7 US-09-727-855B-9
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US-10-425-114-70131
US-10-425-115-359581
US-10-425-115-345444
US-10-424-599-232253
US-10-424-599-23255
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                                                                                                                                                                                                                                      1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                   1 SSQALRIHQWLHLFSDFTST 20
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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106
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Match Length DB
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Maximum DB
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Sequence 45, Apple Sequence 171215, Sequence 17105, Apple Sequence 1876, Apple Sequence 1876, Apple Sequence 1876, Apple Sequence 1876, Apple Sequence 2233, Apple Sequence 24067, Sequence 24067, Sequence 24067, Sequence 24067, Sequence 24067, Sequence 24067, Sequence 226935, Sequence 226935, Sequence 226935, Sequence 18352, Sequence 233087, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3360, Ap
Sequence 264604,
Sequence 176499,
Sequence 145688,
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Sequence 5,
Sequence 6,
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Squence 40. Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alphin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 20
6 US-10-408-765A-2745

5 US-10-424-599-249784

US-10-099-352-43

6 US-10-099-352-43

6 US-10-099-352-43

6 US-10-424-599-171215

US-10-425-115-302525

US-10-425-115-306

US-10-425-115-306

US-10-425-115-306

US-10-425-115-24066

US-10-425-115-24066

US-10-425-115-24066

US-10-425-115-344352

US-10-425-115-344352

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US-10-425-115-24606

US-10-425-115-24606

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US-10-425-115-24606

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US-10-425-115-26406

US-10-425-115-264604

US-10-425-115-264604

US-10-425-115-264604

US-10-425-115-264604

US-10-425-115-264604

US-10-425-115-264604

US-10-425-115-26404

US-10-425-115-26888

US-10-425-115-26888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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     TYPE: PRT

ORGANISM: Homo sapiens
US-10-092-750-40
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Sequence 704, Application US/10412699B Publication No. US20040045049A1
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, James
Fromm, Michael B.
Heard, Jacqueline E.
Riechmann, Jose Luis
Adam, Luc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1055
US-10-412-6998-704
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Samaha, Raymond R.
Pilgrim, Marsha L.
Creelman, Robert A
DuBell, Arnold N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
Yu, Guo-Liang
Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roun, Pierre E.
                                                                                                             Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                        510 SSEGKRLHOWFH 521
                                                                                                                                                                                              1 SSOALRIHOWLH 12
                       FEATURE:
; OTHER INFORMATION: G1055
US-10-302-267-42
                                                                                                                                                                                                                                                                                                                                  US-10-412-699B-704
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                                                                                                                                                                                                                                            d
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Applicant: Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 317501
LENGTH: 132
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Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_52639C.1.pep
WS-10-425-115-317501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FILLEL, SOBERT
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REPERENCE MEI-000.
CURRENT APPLICATION: PLANT GENE SEQUENCES II
FILE REPERENCE MEI-000.
CURRENT APPLICATION NUMBER: US/09/506,720
PRIOR PELING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: G0/120,880
PRIOR FILING DATE: 1999-02-17
PRIOR PELING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: G0/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR PILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-10-22
PRIOR PILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 218
SOFTWARE PARENTH Ver: 2.1
SEQ ID NO 42
LENGTH: 675
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Heard, Jacqueline
Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reuber, Lynne
Zhang, James
Yu, Guo-Liang
Jilang, Cai-Zhong
Samaha, Raymond
Filgrim, Marsha
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Pineda, Omaira
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APPLICANT: Fromm, Michae
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                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2015 SOFTWARE: Patentin version 3.2
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucieotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT FILING DATE: 2003-04-10
PRICR APPLICATION NUMBER: 09/394,519
PRICR FILING DATE: 1999-09-13
PRICR PILING DATE: 2000-01-21
PRICR APPLICATION NUMBER: 09/506,720
PRICR PILING DATE: 2000-01-21
PRICR PILING DATE: 2000-03-22
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44.3%; Score 47; DB 14; Length 675; 58.3%; Pred. No. 85; 3; Indels tive 2; Mismatches 3; Indels
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Patent No. US20020168703A1

GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: HOSHINO, Tatsuo
APPLICANT: SETOGUCHI Yutaka
APPLICANTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUI
TITLE OF INVENTION: MATERIALS THEREOF
FILE REFERENCE: C38435/111694
CURRENT FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 238
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is Gequence 38355, Application US/10425114

is Gequence 38355, Application US/10425114

is Publication No. US20040034888A1

is Publication No. US2004003488A1

is APPLICANT: Liu, Jingdong

is APPLICANT: Zhou, Yihua

is APPLICANT: Tabaska, Jack E

is APPLICANT: Papaska, Jack E

is APPLICANT
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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Pred. No. 87;
3; Mismatches 3
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US-10-425-114-38355
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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Best Local Similarity 80.0%;
Matches 8; Conservative 1
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Best Local Similarity 57.1%;
Matches 8; Conservative
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113 QALDLHQHVHVFPD 126
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ORGANISM: Phaffia rhodozyma
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74 VHQVLHLFSD 83
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-425-114-70131
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; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 341865
; LENGTH: 175
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42.9%; Score.45.5; DB 17; Length 175;
Best Local Similarity 55.0%; Pred. No. 38;
Matches 11; Conservative 3; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                            RESULT 5
103-10-104-047-2357
15 Sequence 2357, Application US/10104047
15 Sequence 2357, Application US/10104047
15 Publication No. US20030236392A1
15 GENERAL INFORMATION:
17 FILE PEPERENCE: HI-A0105
17 TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
17 FILE REFRENCE: HI-A0105
17 CURRENT PELICATION NUMBER: US/10/104,047
18 PRIOR PELICATION NUMBER:
18 PRIOR PELICATION NUMBER:
19 RIGHT PELICATION NUMBER:
10 NUMBER OF SEQ ID NOS: 4096
11 SOFTWARE: PETCHIN OFF: 2.1
18 SEQ ID NO 2357
19 LENGTH: 369
          Query Match
44.3%; Score 47; DB 15; Length 675;
Best Local Similarity 58.3%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 3; Indels
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67;
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US-10-425-115-341865
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Pred. No. 67;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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17 RALRSHRWVSLFS 29
                                                                                                                                                                                             ||: |:|| |
510 SSEGKRLHQWFH 521
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                                                                                                                                                  1 SSOALRIHOWLH 12
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; ORGANISM: Homo sapiens
US-10-104-047-2357
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ORGANISM: Zea mays
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US-09-727-855B-9
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TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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                                           TYPE: PRT
ORGANISM: Zea mays
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US-10-424-599-235750
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      SEQ ID NO 345444
LENGTH: 126
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) Sequence 359581, Application US/10425115
) Publication No. US2004021427241
; GENERAL INFORMATION:
) APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 359381
LENGTH: 83
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Youngei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (52222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70131
LENGTH: 460
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                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: UC-ZMFLB73042B05_FLI.pep
US-10-425-114-70131
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US-10-425-115-359581
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COTHER INFORMATION: unsure at all Xaa locations
FOATURE:
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
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US-10-425-115-34544
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US-10-425-115-359581
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Sequence 23253, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Coard Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement.
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232253
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APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 30-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-44-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 184
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                                                                           Query Match
41.5%; Score 44; DB 17; Length 126;
Best Local Similarity 47.1%; Pred. No. 48;
Matches 8; Conservative 4; Mismatches 5; Indels
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41.5%; Score 44; DB 15; Length 173;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 8; Indels
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US-10-424-599-232253
) OTHER INFORMATION: Clone ID: MRT4577_78212C.1.pep US-10-425-115-345444
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NAME/KEY: unsure
LOCATION: (1)..(184)
PEATURE INFORMATION: unsure at all Xaa locations
PEATURE:
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; Sequence 249784, Application US/10424599
; Publication No. US20040031072A1
; Sendence 249784, Application US/10424599
; Publication No. US20040031072A1
; Sendence 249784
; APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILIS REFERENCE: 38-21 (5323.) B
CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 249784
; LENGTH: 475
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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Glabon, Bradford W.
APPLICANT: Glabon, Bradford W.
APPLICANT: Glann, Gary W.
APPLICANT: Glann, Gary W.
APPLICANT: Glann, Gary W.
APPLICANT: Glann, Gary W.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERBRECE: 660081465;
CURRENT APPLICATION WHERE: US/10/408,765A
CURRENT FILING DATE: 2003-04-04;
NUMBER OF SEQ ID NOS: 3077
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2745
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                                                                 Score 44; DB 15; Length 184;
Pred. No. 69;
3; Mismatches 1; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_67584C.1.pep
US-10-424-599-249784
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54910C.1.pep
US-10-424-599-235750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (1)..(475)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                         RESULT 14
US-10-408-765A-2745
US-10-408-765A-2745
Sequence 2745, Application US/10408765A
Publication No. US20040101874A1
GENERAL INPORMATION:
                                                                 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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||||:|:|:|
70 SQALQISEWMH 80
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CRGANISM: Homo sapiens
US-10-408-765A-2745
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ORGANISM: Glycine max
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Query Match 41.5%; Score 44; DB 15; Length 475; Best Local Similarity 47.1%; Pred. No. 1.8e+02; Matches 8; Conservative 4; Mismatches 5; Indels
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||:| |||: :| : | 189 SSEAFRIHEAIHFCAGF 205 1 SSOALRIHOWLHLFSDF 17

Search completed: November 11, 2004, 01:28:22 Job time: 22.5353 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32 ; Search time 4.45596 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-40 106 1 SSQALRIHQWLHLFSDFTST 20

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\* Database :

1: pir1: \* 3: pir2: \* 4: pir3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			COLUMNIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	46	43.4	272	2	852977	hypothetical prote
0	46	m	275	~	D84769	ical prot
٣	45	•	264	7	T40103	_
4	44		185	7	A70075	ical
'n	44	41.5	1276	7	T09204	11
9	44		1291	~	T09273	Ξ
7	43.5	41.0	164	7	D83172	hypothetical prote
80	43		193	7	A82419	5
0	43	40.6	339	~	E90436	coA-ligase / coenz
10	43	٥.	424	7	C82594	hypothetical prote
11	43		443	(7	297	남
12	43	°.	468	~	AD2395	two-component sens
13	43	ö	534	7	S34679	diphthamide synthe
14	42	39.6	218	N	H69005	hypothetical prote
12	42	9.	253	N	A75159	protein-l-isoaspar
16	42	φ.	292	N	$\alpha$	transcription regu
17	42	φ.	309	N	10	
18	42	39.6	586	N	D82484	SgaT protein VCA02
19	42	ę.	750	7	2	polyketide synthet
20	42	٥.	770	~	F98275	saframycin mx1 syn
21	41	•	144	N	30	hypothetical prote
22	41	38.7	230	~	JC7972	w
23	41	œ.	317	~	H70566	hypothetical prote
24	41		324	N	F69504	proliferating-cell
25	41		340	7	B88939	protein C05E4.11 [
26	41		370	~	-	hypothetical prote
27	41	38.7	396	7	N	hypothetical prote
28	41	38.7	423	7	07	2
29	41	38.7	565	N	S73854	hypothetical prote

hypothetical prote	denome polyprotein	genome polyprotein	hypothetical prote	hypothetical prote	probable 5-carboxy	conserved hypothet	hypothetical prote	probable antioxida	hypothetical prote	hypothetical prote	probable tRNA liga	probable tRNA liga	hypothetical prote	hypothetical prote
T34522	ZLVNSB	ZLVNPV	B96695	C95341	G82048	A75341	E70772	G83215	309896	F64799	F90714	C85565	T15739	AD2269
01 0	٦,	Н	Ŋ	~	7	~	N	~	(7)	(7)	N	N	~	N
568	2127	2142	5138	113	116	181	210	212	214	235	235	235	245	245
r r		7.8	8.7	7.7	7.7	7.7	37.7	17.7	7.7	7.7	7.7	7.7	17.7	37.7
38.7	າຕ	m	m	m	m	(*)	.,,	(,,	"	m	m	m	""	.,
41 38														

## ALIGNMENTS

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Nypothetical protein 3 - Erwinia herbicola (fragment)
C,Species: Erwinia herbicola
C,Species: Erwinia herbicola
C,Species: Erwinia herbicola
C,Bate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C,Accession: 52977
R,Hundle, B.; Alberti, M.; Nievelstein, V.; Beyer, P.; Kleinig, H.; Armstrong, G.A.; Burly
Mol. Gen. Genet. 245, 406-446, 1994
A,Title: Functional assignment of Erwinia herbicola Eho 10 carotenoid genes expressed in A,Reference number: 552976; MulD:95107236; PMID:7808389
A,Accession: 552977
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-272 <HUN>
A,Residues: 1-272 <HUN>
A,Cross-references: UNIPROT:Q01334; EMBL:M87280; NID:g148404; PIDN:AAA64975.1; PID:g14840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 QALRQHRWLCLF 24
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hypothetical protein At2g35500 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004 C;Acession: D84769

William Strain S

· 0 Gaps , 0 Query Match 43.4%; Score 46; DB 2; Length 275; Best Local Similarity 61.5%; Pred. No. 6.9; Matches 8; Conservative 1; Mismatches 4; Indels

6 RIHQWLHLFSDFT 18

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probable tail-host specificity protein - Streptococcus thermophilus phage Sfi21
C;Species: Streptococcus thermophilus phage Sfi21
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T09204
R;Desiere, F.; Bucchini, S.; Brussow, H.
Nirology 241, 345-356, 1998
Nyirile: Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchang A;Reference number: 216607, MUID:98160788; PMID:9499809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable tail-host specificity protein - Streptococcus thermophilus phage Sfi19
() Species: Streptococcus thermophilus phage Sfi19
() Species: Streptococcus thermophilus phage Sfi19
() Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
() Accession: T09273
() B. Descent of Streptococcus thermophilus bacteriophage genomes by modular exchang A; Descent on of Streptococcus thermophilus bacteriophage genomes by modular exchang A; Reference number: 216607; MUID:98160788; PMID:9499809
A; Reference number: Aistorial and A; Reference number: Lanslated from GB/EMBL/DDBJ
A; Residues: 1-1291 cbs>
A; Residues: 1-1291 cbs>
A; Cross-references: UNIPROT:064295; EMBL:AF032122; NID:92935682; PID:92935691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA3780 [imported] - Pseudomonas aeruginosa (strain PACI)
Cispecies: Pseudomonas aeruginosa
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
CiAccession: D83172
Riscover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bridan, S.; Yuun, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1276 <DES>
A;Cross-references: UNIPROT:O64284; EMBL:AF032121; NID:g293567; PID:g2935676
C;Keywords: tail protein
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                    Length 185;
                                                                                                                                                                                                                                   Indels
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                                     A,Gene: yxeG
C,Superfamily: Bacillus subtilis hypothetical protein yxeG
                                                                                                                                                Query Match 41.5%; Score 44; DB 2; Best Local Similarity 41.7%; Pred. No. 9.5; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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Pred. No. 77;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2
Pred. No. 76;
3; Mismatches
                                                                                                                                                                                                                                                                                                              5 LRIHQWL-----HLFSDFT 18
                                                                                                                                                                                                                                                                                                                                                           41.5%;
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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Matches 7; Conservative
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C;Genetics:
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Cippecies: Broughlet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujtta, M.; Fujtta, Y.; Fuma, S.; Galler, C.; Ferrari, E.
Nature 300, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujtta, M.; Fujtta, Y.; Puma, S.; Galler, A.; Landwod, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapddus, A.; Lardinois, A.; Liu, H.; Masuda, S.; Maueell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portot, A.; Athores: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiquchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 1-264 <BAR>
A)Residues: 1-264 <BAR>
A)Cross-references: UNIPROT:074796; EMBL:AL049495; PIDN:CAB39854.1; GSPDB:GN00066; SPDB:A)Cross-references: UNIPROT:074796; cosmid c2A9 3p
B)Body V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
R;Wood, V.; Rajandream, M.A.; Berrell, B.G.; Taylor, K.; Harris, D.
A)Reference number: 221906
A)Accession: T40105
A)Status; preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:D54946; GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB15992.
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-764 <WOO>
A;Residues: 1-764 <WOO>
A;Cross-references: EMBL:AL031788; PIDN:CAA21160.1; GSPDB:GN00067; SPDB:SPBC2D10.02
A;Experimental source: strain 972h-; cosmid c2D10
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                                                                                                                                                                                          hypothetical protein SPBC2D10.02 - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Gene. SPEC2D10.02
A;Map position: 2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC2D10.02
                                                                                                                                                                                                                                                                                                     C;Accession: T4103; T40105
R;Barrell, B G.; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher,
Bubmitted to the EMBL Data Library, March 1999
A;Reference number: Z21905
A;Accession: T40103
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42.5%; Score 45; DB 2;
Best Local Similarity 43.8%; Pred. No. 9.6;
Matches 7; Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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181 TSSALQIQYWMHVLSE 196
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    192 RADQWRHLYSGFT 204
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A;Gene: SPBC2A9.12
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A;Introns: 61/2

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Libory, S.; Olson, M.V. Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Brody, S.; Olson, M.V. Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. Mature enumber: Age-9594, D.D.; Multiple: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: Age-9595, MUD: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: D82975
A,Status: preliminary
A,Molecus: preliminary
A,Residues: L-443 <STO>
A,Cross-references: UNIPROT:P23621; GB:AE004948; GB:AE004091; NID:g9951680; PIDN:AAG08746
A,Experimental source: strain PAO1
C,Genetics:
C,Genetics:
C,Superfamily: phosphate regular regulatory protein; sensor histidine kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyaccession: C82594 Target Agriculture of the Organization for Nucleotide Sequence Astronymous The Xytella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Title: The genome Sequence of the plant pathogen Xylella fastidiosa.
A,Title: The Genome Sequence of the plant pathogen Xylella fastidiosa.
A,Notes: for a complete list of authors see reference number A59328 below
A,Accession: C82594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein XF2151 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                           Length 339
                                                                                                                          0; Indels
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Pred. No. 34;
4; Mismatches
     DB 7
                      Score 43; DB 2
Pred. No. 26;
4; Mismatches
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53.8%;
                           40.6%;
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                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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171 HEWLHIWTD 179
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Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, A,Reference number: A82950; MUD:20437337; PMID:10984043
A,Reference numbar: D83172
A,Status: preliminary
A,Roleolie type: DNA
A,Residues: 1-164 < STO>
A,Cross-references: UNIPROT:Q9HXL5, GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG0716
C,Genetics: A,Residues: L-164 & STO>
A,Cross-references: UNIPROT:Q9HXL5, GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG0716
C,Genetics: A,Residues: A,R
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B90436
C.0A-ligase / coenzyme F390 synthetase, probable [imported] - Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: B90436
R; Ahore 20: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: B90436
A; Status: preliminary
A; Retere DNA
A; Reserve 
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A,Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical protein VCA0769 [imported] - Vibrio cholerae (strain N16961 sero; Cispecies: Vibrio cholerae
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Accession: A82419
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Aridelberg, J.F.; Eisen, J.A.; Namethevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Feference number: A82035; MuID:20406833; PMID:10952301
A;Accession: A82419
A;Accession: A82
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A,Crosa-references: UNIPROT:097VJ6; GB:AE006641; NID:gl3815936; PIDN:AAK42748.1; GSPDB:
C,Genetics:
A,Gene: SSO2627
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Pred. No. 14;
6; Mismatches 3; Indels
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41.0%; Score 43.5; D
Best Local Similarity 41.7%; Pred. No. 10;
Matches 10; Conservative 5; Mismatches
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A;Map position: 2
C;Superfamily: Escherichia coli yajB protein
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Best Local Similarity 35.7%;
Matches 5; Conservative
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QGIRLHRWVDAYTD 53
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A;Cross-references: EMBL:228191; NID:g486338; PIDN:CAA82035.1; PID:g486339; MIPS:YKL191w A;Cross-references: EMBL:228191; NID:g486338; P.; Rimaia e Silva, A.; Bossier, P.; Vilela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; Rc submitted to the Protein Sequence Database, March 1994 A;Reference number: S38024 A;Accession: S38028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein MTH1040 - Methanobacterium thermoautotrophicum (strain Delta H)
hypotheteies: Methanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum
C.Sacterium thermoautotrophicum
C.Sacterium thermoautotrophicum Delta H: functi
A.Tille: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A.Reference number: A69000, MuID:98037514; PMID:9371463
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A;Experimental source: strain Delta H
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-534 <MAI>
A;Cross-references: EMBL:Z28191; NID:g486338; PIDN:CAA82035.1; PID:g486339; MIPS:YKL191w
R;Pardo, J.M.
A;Cross-references: GB:L01424; NID:g171413; PIDN:AAA64990.1; PID:g765109
R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, submitted to the Protein Sequence Database, March 1994
A;Reference number: S37825
A;Accession: S38023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1993
A)Description: The protein phosphatase calcineurin is essential for NaCl tolerance in A)Reference number: S52281
A)Reference number: S52281
A)Residues: S5234
A)Residues: 256-534
A)Residues: 256-534
A)Residues: EMBL:226521; NID:g473144; PIDN:CAA81289.1; PID:g473145
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A;Residues: 1-218 <MTH>
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24;
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55.6%; Pred. No. 24;
tive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SGD:DPH2
A;Cross-references: SGD:S0001674; MIPS:YKL191w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.6%; Score 43;
ilarity 50.0%; Pred. No. .
Conservative 2; Mismatcl
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C;Keywords: diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSOALRIHOWLHLFSDFTST
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nes 10; Conserv
                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-534 <WI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Two-component sensor histidine kinase alr4716 [imported] - Nostoc sp. (strain PCC 7120) G;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
G;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2395
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:2159285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molcoule type: DNA
A,Residues: 1-468 «KUR»
A,Cross-references: UNIPROT:Q8YN54; GB:BA000019; PIDN:BAB76415.1; PID:g17133853; GSPDB:G
A,Experimental source: strain PCC 7120
C;Genetics:
A,Gene: a1r4716
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A.Residues: 1-534 (WIE>
A.Cross-references: UNTROT.P32461, EMBL:X74151; NID:g450365; PIDN:CAA52247.1; PID:g3952
A.Note: the published sequence was revised in GenBank
R.Cheret, G.; Mattheakis, L.C.; Sor, F.
Yeast 9, 661-667, 1993
A.Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cere
A.Reference number: S33960; MUID:93348778; PMID:8394042
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A; Readdues: 1.534 cCH8.
A; Cross-references: GB:X69765; NID:g296985; PIDN:CAA49420.1; PID:g296987
A; Mattheakis, L.C.; Sor, F.; Collier, R.J.
Gene 132, 149-1154, 1993
A; Title: Dibthamide synthesis in Saccharomyces cerevisiae: Structure of the DPH2 gene.
A; Reference number: JN0855; MUID:94010339; PMID:8406038
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                                                           Score 43; DB 2;
Pred. No. 35;
1; Mismatches
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Pred. No. 37;
0; Mismatches
                                                               40.68;
77.88;
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87.5%;
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                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-534 <MAT>
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Matches

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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75159
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strut A;Accession: A7519
A;Accession: A7519
A;Accession: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strut A;Accession: Dylanary
A;Accession: Bylanary
A;Gratus: preliminary
A;Gratus: 1-253 «KAW>
A;Acsidus: 1-253 «KAW>
A;Accession: Bylanary
A;Cross-references: UNIPROT:O9VJJ7; GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB4935
C;Genetics:
A;Gene: pimT-like; PAB0283
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Search completed: November 10, 2004, 13:40:48 Job time: 5.45596 secs

1 SSQALRIHQWIHLFSDF 17 |:|:|:|:| 197 SNQVMRLHEKLREFKDY 213

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Butaleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Douglas S.E., Gallant J.W., Bullerwell C.E.;

Douglas S.E., Gallant J.W., Bullerwell C.E.;

Molecular Investigation of Aminopeptidase N Expression in the Winl Flounder, Pleutonectes americanus.";

J. Appl. Ichthyol. 0:0-0(1998).

R. EMBL, ARGA32807.1;

R. GO; GO:0004177; F:aminopeptidase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

R. GO; GO:0016787; F:hydrolase activity; IEA.

R. GO; GO:0016787; F:hydrolase MI.

InterPro; IPR001930; Peptidase MI.

InterPro; IPR001930; Peptidase MI.

R. PRINTS; PR01433; Peptidase MI.

R. PRINTS; PR01413; Peptidase MI.

R. PRINTS; PR01413; ZINC_PR07EASE; UNKNOWN_I.

M. Aminopeptidase; Hydrolase.

T. NON_TER.
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Pred. No. 19;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Aminopeptidase N (EC 3.4.11.2) (Fragment).
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Aminopeptidase N (EC 3.4.11.2).
                                                                                                                                                                                                                                                                                               680 AA
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VAPD NEIGO
Q6ZKQ8
Q9UUT1
Q9C148
Q7C148
Q8IJ31
Q8IJ31
Q8EGF3
Q64284
Q64295
Q754A3
AASS3540
Q9HXL5
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01-MAY-2000 (TrEMBLrel. 13, Created)
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Q8svu0 encephalito
Q8ei96 shewanella
Q8484 oryza sativ
Q7pp27 anopheles g
Q8w029 arabidopsis
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Q89Ju4 arabidopsis
Q99G6 arabidopsis
Q01334 erwinia her
Q9136 arabidopsis
Q61239 arabidopsis
Q6bu20 debaryomyce
Q6159 australian
Q6149 canis famil
Q6141 canis famil
Aar87835 canis famil
Aar87835 canis famil
Aar87836 canis famil
Q62008 homo sapien
Bac86171 homo sapien
G89308 ralstonia s
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Q73dk9 treponema
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                                                                                             November 10, 2004, 12:27:34 ; Search time 24.4214 Seconds
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                   protein search, using sw model
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1 SSQALRIHOWLHLFSDFTST
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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InterPro, IPR004340; UL52 UL70. Pfam; PF03121; Herpes_UL52; 1.
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                                           Helicase.
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Douglas S.E., Gallant J.W., Bullerwell C.E.;
"Molecular Investigation of Aminopeptidase N Expression in the Winter Flounder, Pleuronectes americanus.";
J. Appl. Ichthyol. 0:0-0(1998).
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                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, setinoptearygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes, Pleuronectoidei, Pleuronectidae, Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20578232; PubMed=11134310;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Rock D.L., Kutish G.P.,
"The genome of turkey herpesvirus.";
J. Virol. 75:971-978(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Journal of herpesvirus of turkeys: comparative analysis with Marek's disease viruses.";
J. Gen. virol. 82:1123-1135 (2001).
EMBL, AF291866, AAG45790.1;
EMBL, AF28130; AAG30093.1;
EMBL, AF28186; F:DNA Primase activity; IEA.
GO, GO:0003896; F:DNA Primase activity; IEA.
GO, GO:0004866; F:DNA replication; IEA.
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                          Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
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Kingham B.F., Zelnik V., Kopacek J., Majerciak V., Ney E.,
Schmidt C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 51; DB 2; Length 974; 80.0%; Pred. No. 27; ive 1; Mismatches 1; Indels
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OI-MAR-2001 (TrEMBLrel. 16, Last sequence update)
OI-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E Holicase-primase associated protein (UL52 DNA helicase-primase associated protein (UL52 DNA helicase-primase protein).
Name-HVT060; SYDONYMS-UL52;
S Meleagrid herpesvirus 1 (herpesvirus of turkeys).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaharpesvirinae; Marek's disease-like viruses.
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PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
Aminopeptidase; Hydrolase.
SEQUENCE 974 AA; 109743 MW; ECE551C9488!
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EMBL; AF012465; AAC32754.1; -.
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                                                    americanus)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Name=ECU04_0880;
Bncephalitozoon cuniculi.
Bukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALS90444; CAD25275.1; -
GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IBA.
GO; GO:0006783; P:heme biosynthesis; IEA.
InterPro; IPR003754; HEM4_synth.
                                             Length 1078;
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1078 AA; 120951 MW; AA1F10CF511BDF65 CRC64;
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SEQUENCE 192 AA; 22306 MW; PAF2E41DD91D0B31 CRC64;
                                                                                                                                                                                                                                                                                                                                      Q8SVUO;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-YAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein ECU04_0880.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-dependent RNA helicase SrmB.
Name=srmB. OrderedLocusNames=S00947;
Shewanella oneidensis
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46.7%; Pred. No. 15;
ative 5; Mismatches
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                                                46.2%; Score 49; DB 47.1%; Pred. No. 64;
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Best Local Similarity 63.0.
Best Local 7; Conservative
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Best Local Similarity 50.0
Matches , 8; Conservative
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MEDLINE-22297686; PubMed=12368813; DOI=10.1038/nbt749;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Elsen J.A., Seshadri R., Ward N.L., Methe B.A.,
Clayton R.A., Meyer T., Tappin A., Scott J., Beanan M.J.
Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprain M.,
Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
Venter J.C., Nealson K.H., Fraser C.M.;
'Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrnartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                        Nat. Biotechnol. 20:1118-1123(2002).
-1- SIMILARITY: Belongs to the DEAD box helicase family.
EMBL; AE015540; AAN54021.1; -.
HSSP; P10081; 1QDE.
                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005524; F:ATP binding; IEA.
GO:0008026; F:ATP-dependent helicase activity; IEA.
GO: GO:0016787; F:hydrolase activity; IEA.
GO: GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00039; DEAD ATP HELICASE; 1.
ATP-binding; Complete proteome; Helicase; Hydrolase.
SEQUENCE 420 AA; 46809 MW; CSF83898314E38F8 CRC64;
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InterPro; IPR011545; DEAD/DEAH_N.
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InterPro; IPR001650; Helicase_C.
Pfam; PP00270; DEAD; 1.
SPART; SM00497; Helicase_C; 1.
SMART; SM00497; DEXDC; 1.
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Name=P0014E04.8;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-AtbZIP28;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
"The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
Babli, Apolis2; BACS5975.1; -.
Gramene, Q845K4; -.
SEQUENCE 78 AA; 8527 MW; 4112738P1B770850 CRC64;
                                                                                                                                                                                     44.3%; Score 47; DB 2; Length 78; 50.0%; Pred. No. 8; cive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 AA; 23197 MW; 12DE4512C1ECB614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=11481677; PubMed=11597504;
Stracke R., Werber M., Weisshaar B.;
"The R2R3-MYB gene family in Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO0000021244 (Fragment).
Name-ENSANGG0000018755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.

EMBL; AAABO1008960; EAA11128.2; -...
GO; GO1005509; F:calcium ion binding; IEA.
InterPro; IFR002048; EF-hand.
Pfam; PF00036; efhand; 3.
ProDom; PD000012; EF-hand; 2.
PROSITE; PS00018; EF-HAND; UNKNOWN.
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01-MAR-2002 (TrEMBLrel. 20, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annot
AtbZIP transcription factor (Fragment)
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01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
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Matches 7; Conservative
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                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=At3g10800;
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Q9SG86;
                                                                                                                                                                                                                                                   Q8GUH4
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MEDILINE=22022145; PubMed=12024217;

MEDILINE=22022145; PubMed=12024217;

A silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

A loves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A loves L.M.C., Cannavan F., Cardozo J., Chambergo F., Ciapina L.D.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.D.,

A camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.D.,

A caralli R.M.B., Couttinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A caralli B.C., Machado M.J., Madeira R.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,

A spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

A setubal J.C., Kitajima J.P.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering J.P.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Chiveira V.F.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Chiveira V.F.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Chiveira V.F.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Chiveira V.F.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Textering M.C., Textering M.C., Chiveira V.F.,

A setubal J.C., Kitajima J.P.,

North Spinola L.A.F., Textering M.C., Textering 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas axonopodis (pv. citri),
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.3%; Score 47; DB 2; Length 326; llarity 58.3%; Pred. No. 37; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Jakoby M.J.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ419860; CAD12033.1; -.
1 1
SEQÜENCE 326 AA; 34980 MW; 6A60B3C155BE9D9C CRC64;
                                                                                                                         MEDLINE=20249261; PubMed=1078565; Stracke R., Werbber M., Weissbaar B.; Stracke R., Werbber M., Weissbaar B.; "The WRKY superfamily of plant transcription factors."; Trends Plant Sci. 5:199-206(2000).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.3%; Score 47; DB 2; 37.9%; Pred. No. 57;
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        Curr. Opin. Plant Biol. 4:447-456(2001)
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EMBL, AE012009; AAM38432.1; -.
GO, GO.0016020; C:membrane; IEA.

InterPro; IPR000150; Hypothet cof.

InterPro; IPR000537; UbiA_premyltrans.
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PROSITE; PS01228; COF_1; UNKNOWN_1.
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OrderedLocusNames=XAC3589;
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Best Local Similarity 3/...
Local 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 481 AA;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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01-0CT-2002
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Q8PGM7
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3 QALRIHQWL------HLFSDFTS 19

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RA SOUTHWICK A. WOUNGEN M. Tripp M., Palm C.J., Jones T., Wu T.,

RA Southwick A. Winyen M., Tripp M., Palm C.J., Jones T., Wu T.,

RA Carnici P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

RA Dang J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kantani R.,

RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,

RA Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,

RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,

RA Davis R.W.;

Bubmitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

C. !- SIMILIANTY: Belongs to the BZIP family.

CR SIME, BT002502; AA000662.1; --

CR GO, GO.000534; C.nucleus; IEA.

GO, GO.000537; Piragulation of transcription, DNA-dependent; IEA.

RICEPERO, IPRO0837; FI-BZIP.

RICEPERO, IPRO0838; BRLZ; I.

RICEPERO, IPRO0838; BRLZ; I.

RWART; SMO0338; BRLZ; I.

RWART; SMO0338; BRLZ; I.

RWART; SMO0338; RGC64; SEQUENCE 675 AA; 73460 WW; 953B29B12A762F85 CRC64;
                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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- I-SIMILARITY: Belongs to the bZIP family.

EMBL; AC011708; AAF19569.1; --
GO, GO:0005634; C:nucleus; IEA.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Putative bZIP transcription factor.
Name=T7M13.12;
               01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Nutative bZIP transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.3%; Score 47; DB 2;
58.3%; Pred. No. 82;
tive 2; Mismatches
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Created)
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Matches

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Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Expressed protein (At2g35500/T32F12.12).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Enbryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Exassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang B., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamadad K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Shounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M., Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.4%; Score 46; DB 2; Length 353; 50.0%; Pred. No. 59; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Town C.D., Kaul S.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mortimore BJ.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
353 Aa; 41033 MW; D6DC67E0DD875A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GO; GO:0016787; F:hydrolase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR004843; M.pesterase.
Pfam; PF00149; Metallophos; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
            protein H25K10.1.
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                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
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Matches
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082290
            DDR REP REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BRY REP BR
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hundle B., Alberti M., Nievelstein V., Beyer P., Kleinig H., Armstrong G.A., Burke D.H., Hearst J.E.; Functional assignment of Erwinia herbicola Bholo carotenoid genes expressed in Escherichia coli: "; Mol. Gen. Genet. 245:406-416(1994).
GO; GO:0003677; F:DNA binding; IEA.

GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR004917; EUK transcr_DNA.

InterPro; IPR004827; TF_EZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxID=549;
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                                                                                                                                                                                                                                                                                            44.3%; Score 47; DB 2; Length 675; 58.3%; Pred. No. 82; ive 2; Mismatches 3; Indels
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                                                                                               Incertic, Account of Date; 1.
SMART; SM00338; BRLZ; 1.
PROSITE; PS50217; BZIP; 1.
DNA-binding; Nuclear protein.
SEQUENCE 675 AA; 73432 MW; DAA74401C581C078 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001927; Na/Gal symport.
PROSITE; PS00072; Na_GALACTOSIDE_SYMP; FALSE_NEG.
Hypothetical protein.
SEQUENCE 272 Aa; 29955 MW; C7C7538416F14AB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical 29.9 kDa protein in crtE 3'region (ORF3).
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Last annotation update)
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MEDLINE=95107236; PubMed=7808389;
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les 7; Conservative
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01-MAY-2000 (
01-JUN-2003 (
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Q01334;
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Q9U3D3;
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,

Boistame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

A Boistame A., Robre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Rellenz S., Pociter S., Richard G.F., Straub M.L., Suleau A.,

Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Mirth B.,

Zenjou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.L.;

Mincker P., Souciet J.L.;

I. Nature 430:35-44(2004).
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CAll56 [CARLRI Candida albicans.
ORFNames=DEHAOC07601g;
ORFNames=DEHAOC07601g;
Comycoe hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaces; Debaryomyces.
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                                                                                                                                                                                                                                                                                                                                                 43.4%; Score 46; DB 2; Length 387; 61.5%; Pred. No. 65; 4; Indels ative
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR892135; CAG86037.1; -.
SEQUENCE 1581 AA; 182145 WW; DEFF4AAB263B32E8 CRC64;
                                                                                                                 (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 Interpro; IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
SEQUENCE 387 AA; 42687 MW; CF784D442E76503A CRC64;
                                                                                                                              PRT; 1581 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 RADOWRHLYSGFT 283
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Matches 8; Conservative
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STRAIN=CBS767;
GENOLEVURES;
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                                                                                                   Ecker J.R.;
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Q6BUZ0
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Gaps .

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Best\_Local Similarity 58.3 Matches 7; Conservative

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Search completed: November 10, 2004, 13:38:46 Job time: 26.4214 secs
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536 RKHEWLHYFRNF 547
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6 RIHOWLHLFSDF 17

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14:55:24 2004
Fri Nov 12
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Query Match
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                                                                                                 November 10, 2004, 12:32:37; Search time 6.21762 Seconds (without alignments) 191.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents AA:*

.. /cgn2 6/ptodata1/liaa/5A_COMB.pep:*
.. /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
.. /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
.. /cgn2 6/ptodata1/liaa/6B_COMB.pep:*
.. /cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
.. /cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-24-364-364-36
US-09-24-364-36
US-08-440-391-2
US-08-440-391-18
US-08-908-597A-12
US-08-908-597A-12
US-08-908-597A-12
US-09-236-385A-2
US-09-236-385A-2
US-08-31-14
US-08-908-597A-14
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US-08-9771-058-9
US-08-9771-058-10
                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           478139 segs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             1 GQVGRQLAIIGDDINRRK 18
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Maximum DB seq length: 200000000
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90
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Match
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Perfect score:
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No.
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CITY: nac.....
STATE: D.C.
ZIP: 2000BUCTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25
CURRIT APPLICATION DATA:
FLING DATE: 2-Jan.1999
CLASSIFICATION: VUNRIOWN>
APPLICATION: VUNRIOWN>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acid
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%; Score 85; DB 3; Length 19; 100.0%; Pred. No. 1.5e-08; ative 0; Mismatches 0; Indels
           US-08-471-057-9

US-08-471-057-10

US-08-471-057-11

US-08-471-0865-7

US-08-470-865-10

US-08-470-865-11

US-08-470-865-11

US-09-155-3276-13

US-09-544-664B-5

US-08-440-391-3

US-08-440-391-3

US-08-440-391-3

US-08-908-597A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/09236385A Patent No. 6221615 GENERAL INFORMATION:
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Matches 17; Conserv
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ORGANISM: Artificial Sequence
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US-08-440-391-2
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REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEPHONE: 202-942-8440
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%; Score 85; DB 3; Length 20; 100.0%; Pred. No. 1.6e-08; Live 0; Mismatches 0; Indels
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APPLICANT: Wang, Jialun
APPLICANT: Wang, Jialun
APPLICANT: Zhang, Zhijia
APPLICANT: Zhang, Zhijia
APPLICANT: Lu, Zhixian
APPLICANT: Lu, Zhixian
APPLICANT: Lu, Zhixian
APPLICANT: Lu, Zhixian
APPLICANT: Lu, Zhixian
APPLICANT: Zhixian
CURRENT APPLICANTON NUMBER: US/09/544,664B
CURRENT FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                      COMPUTATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 25-385A
FILING DATE: 25-301-1999
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
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PRIOR FILING DATE: 2000-04-06
PRIOR PELLING DATE: 2000-04-07
PRIOR PILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 58
SOTTWARE: Patentin Ver. 2.1
SEQ ID NO 4
INNOTED NO 5
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36
                                                Sequence 36, Application US/09236385A Patent No. 6221615 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 41
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Best Local Similarity 100.0
Warches 17; Conservative
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                                  -09-236-385A-36
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CTHER INFORMATION: Description of Artificial Sequence: Peptide OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily CTHER INFORMATION: polypeptide US-09-544-6648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08440391

Batent No. 5656725

GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ. Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Hale and Dorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL PEPTIDES AND COMPOSITIONS WHICH
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                                                                                                                      Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIPATE: D.C.
ZIPATE: D.C.
ZONO4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MA-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/LOCKET NUMBER: 104322.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 85; DB 1; Le
Pred. No. 2.3e-08;
                                                                                                                 Query Match
94.4%; Score 85; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0;
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US-08-440-391-18
US-08-440-391-18
; Sequence 18, Application US/08440391
; Patent No. 5656725
; Patent No. 5656725
; APPLICANT: CHITTENDEN, Thomas D.; and ; APPLICANT: LUTZ, ROBert J.
TITLE OF INVENTION: NOVEL PEPTIDES ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Sc.
100.0%; Pred
0; N
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TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GQVGRQLAIIGDDINRR 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear / MOLECULE TYPE: peptide US-08-440-391-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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18-10-032-/30-41.TA1
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Length 28;
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                                                                                                                                                                                                                                                                                               Query Match 94.4%; Score 85; DB 2; L. Best Local Similarity 100.0%; Pred. No. 2.3e-08; Matches 17; Conservative 0; Mismatches 0;
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                                 TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 5.
SEQUENCE CHARACTERISTICS:
LENGTH: 28 aming acid
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-908-597A-18
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US-08-908-597A-2

Squence 2, Application US/08908597A

Squence 2, Application US/08908597A

Squence 2, Application US/08908597A

Squence 2, Application US/08908597A

APPLICANT: CHITENDEN, Thomas D.; and APPLICANT: CHITENDEN, Thomas D.; and APPLICANT: CHITENDEN, Thomas D.; and APPLICANT: CHITENDEN, NOVEL PEPTIDES AND COMPOSITIONS WHICH TILE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS: 34

CORRESPONDENCE ADDRESS:
ADDRESSES: Hale and Dorr STREET: 1455 Pennsylvania Avenue, N.W.

STREET: 1455 Pennsylvania Avenue, N.W.

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A

FILING DATE: 12-MAY-1995

ATPLING DATE: 12-MAY-1995

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.4%; Score 85; DB 1; Length 28; 100.0%; Pred. No. 2.3e-08; tive 0; Mismatches 0; Indels
                                          CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Waahington
CITY: Waahington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION NUMBER: 104322.147
FILERAX: 202-942-8400
TELEPRAN: 202-942-8400
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: minoaride
TITLE OF INVENTION: MODULATE APOPTOSIS NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GOVGROLATIGDDÍNRR 22
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear;
// MOLECULE TYPE: peptide US-08-440-391-18
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Fri Nov 12 14:55:24 2004

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Query Match

94.4%; Score 85; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.1471
TELEPHONE: 202-942-8400
                      ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
FEBRUARY SEQUENCE 2, Application PC/TUS9606122
; GENERAL INFORMATION 1NC
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GOVGRQLAIIGDDINRR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-06122-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
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Sequence 18, Application US/09236385A
Setent No. 6221615
GENERAL INFORMATION:
CHITTENDEN, Thomas D.; and
APPLICANT: CHITTENDEN, Thomas D.; and
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                              APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: WOULD PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.4%; Score 85; DB 3; Length 28; Best Local Similarity 100.0%; Pred. No. 2.3e-08; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 25-Jan-1999
FILING DATE: 25-Jan-1999
                                                                                                                                                                                                                                                                                                                                           ZIP: 20004

COMPUTER READLABLE FORM:

COMPUTER: FLORPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION MADRER: US/09/236,385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-236-385A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
                            Sequence 2, Application US/09236385A Patent No. 6221615
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GOVGRQLAIIGDDINRR 17
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                                                                                                                                                                                                    NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-236-385A-18
          US-09-236-385A-2
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(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HERBWITH
CLASSIFICATION: NUMBER: PCT/US96/06122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: WORLE PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE 3.34
CORRESPONDENCE ADDRESS:
ADDRESSEE: 444e and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104322.147PCT
                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-236-385A-18
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WESTORY 13

US-08-908-597A-14

i Sequence 14, Application US/08908597A

i Sequence 14, Application US/08908597A

i Patent No. 5863795

i GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: UTZ, ROBERT J.

ITILE OF INVENTION: MODILATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and DOXT

STARE: 12004

CITY: Washington

STARE: Poper Sequence, N.W.

CITY: Washington

STARE: Poper Sequence, N.W.

CITY: Washington

STARE: Poper Sequence

CITY: Poper SEQUENCES:
CORRESPONDENCE FORM:

MEDIUM TYPE: Floppy disk

CORPUTER READABLE FORM:

MEDIUM TYPE: Poper Sequence

CORREST PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CLASSIFICATION NUMBER: US/08/440,391

FILING DATE: 12-MAY-1995

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147

TELECOMMUNICATION NUMBER: 104322.147

TELECOMMUNICATION NUMBER: 104322.147

TELECOMMUNICATION NUMBER: 104322.147

TELECOMMUNICATION NUMBER: 104322.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%; Score 85; DB 1; Length 36; 100.0%; Pred. No. 3.1e-08; Live 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MA-1995
CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 32,073
RELEPARIONE 202-942-8400
TELEPAR: 202-942-8404
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
LEMOTH: 36 base pairs
mvnp: anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito anito a
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Best Local Similarity 100.0
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-5908-597A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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| Sequence 14, Application US/08440391
| Patent No. 5656725
| GENERAL INFORMATION:
| APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, ROBER J.
| TITLE OF INVENTION: MODULATE APOPTOSIS
| TITLE OF INVENTION: MODULATE APOPTOSIS
| NUMBER OF SEQUENCES: 34
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Hale and Dorr | STREET: 1455 Pennsylvania Avenue, N.W. | CITY: Washington | STREET: 20004
| STAPE: 20004
| COMPUTER READABLE FORM: | MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                 PETUTION TILE
PETUTION TILE
PETUTION TILE
SEQUENCE 18, Application PC/TUS9606122
GENERAL INFORMATION:
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
INTERED TO SECUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 145 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: 0.C.
ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENTION:
PRILICATION NUMBER: DCT/US96/06122
FILING DATE: 12-MAY-1995
CLASSIFICATION:
PRICATION NUMBER: US 08/440,391
FILING DATE: L2-MAY-1995
CLASSIFICATION NUMBER: 12-MAY-1995
FILING DATE: 12-MAY-1995
CLASSIFICATION NUMBER: 32,073
RESTERRING NUMBER: 32,073
RESTERRING NUMBER: 130,073
RESTERRING NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
NAME: WIXON, HERRY N.
FERERRENGE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 2.3e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 10 NO: 18: SEQUENCE CHARACTERISTICS: ENUTY: 28 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide PCT-US96-06122-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GOVGROLAIIGDDINRR 22
             6 GOVGRQLAIIGDDINRR 22
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US-08-440-391-14
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PCT-US96-06122-14
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                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:

ADDRESSE: Hale and Dorr
STRET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DEARLIN PC-DOS/MS-DOS
SOFTWARE: 25-Jan.-1999
CLASSIFICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan.-1999
CLASSIFICATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEPHONE: 202-942-8400
TELEPHONE: 202-942-8400
TELEPHONE: CHARACTERISTICS:
LENGTH 36 base pairs
TWODE: amino anid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                APPLICANT: CHITTENDEN, Thomas D.; and LUTZ, Robert J. TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
       Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 36;
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Sequence 14, Application PC/TUS9606122

GENERAL INFORMATION:
APPLICANT: INMUNOGEN, INC.
ITLE OF INVENTION: WHICH MODULATE APOPTOSIS
ITLE OF INVENTION: WHICH MODULATE APOPTOSIS
ITLE OF SEQUENCES: 34
CORRESPONDERSED: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
STREET: D.C.
94.4%; Score 85; DB 2; Le
ilarity 100.0%; Pred. No. 3.1e-08;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
94.4%; Score 85; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-236-385A-14
                                                                                                                                                                                                   RESULT 14
US-09-236-385A-14
Sequence 14, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
                                                                                            1 GOVGROLAIIGDDINRR 17
                                                                                                                                      8 GOVGROLAIIGDDINRR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GOVGRQLAIIGDDINRR 17
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
COMPUTER: IB PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION UNDER: PCT/US96/06122
FILING DAME: HERBWITH
CLASSIFICATION:
PRIOR APPLICATION UNDER: US 08/440,391
FILING DAME: 12-MAX-1995
CLASSIFICATION:
MACSIFICATION:
ATTORNEY/AGRIT INFORMATION:
MASSIFICATION:
REPERENCE/DOCKET NUMBER: 10,432.147PCT
TELECOMMUNICATION INFORMATION:
MASSIFICATION:
REPERENCE/DOCKET NUMBER: 10,432.147PCT
TELECOMMUNICATION INFORMATION: 14:
FELECOMMUNICATION INFORMATION: 14:
FELECOMMUNICATION INFORMATION: 14:
FELECOMMUNICATION OR SEQ 10 No. 14:
FELECOMMUNICATION POR NO. 14:
FELECOMMUNICATION POR NO. 14:
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FELECOMMUNICATION POR NO. 14:
FELECOMMUNICATION POR NO. 14:
FELECOMMUNICATION P
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.; 0 Sequence 2, Appli Sequence 5, Appli Sequence 73, Appli Sequence 3, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 11, Appli Sequence 10, Appli Sequence 20, Appli Sequence 27, Appli Sequence 26, Appli Sequence 25, Appli

Sequence 7551, A Sequence 10076, A Sequence 741, App Sequence 43390, A Sequence 13718, A

US-10-369-493-741 US-10-282-122A-43390 US-09-815-242-13718

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Gaps

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100.0%; Score 90; DB 14; Length 18; 100.0%; Pred. No. 5.7e-08; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10092750; Sequence 2, Application US/10092750; Publication No. USZ0030032157A1; GENERAL INFORMATION; Publication No. USZ0030032157A1; GENERAL INFORMATION; Philip W.; APPLICANT: Alpin, Julia APPLICANT: Wright, Martin C.; TITLE OF INVENTION: POLYpeptides Interactive with BCL-X1; FILE REFRENCE: 50036/050002; CURRENT APPLICATION NUMBER: US/10/092,750; CURRENT FILING DATE: 2002-03-07; PRIOR PILING DATE: 2001-03-08; NUMBER OF SEQ ID NOS: 253; SOFFWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2: LENGTH: 18
4 US-10-189-294-2

4 US-10-03-632C-6

0 US-09-840 085-73

4 US-10-059-261-240

7 US-10-059-261-240

4 US-10-052-760-240

4 US-10-092-750-240

4 US-10-092-750-156-9

4 US-10-092-750-140

1 US-09-828-870-3

1 US-09-828-870-16

US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-10

1 US-09-828-870-30

1 US-09-912-599-18

2 US-10-259-18

1 US-09-912-599-8

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US-10-092-750-41
Sequence 41, Application US/10092750
Publication No. US20030032157A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GQVGRQLAIIGDDINRRK 18
 Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-2
    US-10-092-750-2
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Sequence 35, Appl
Sequence 36, Appl
Sequence 36, Appli
Sequence 18, Appli
Sequence 14, Appli
Sequence 22, Appli
Sequence 27, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
                                                                                                                   (without alignments)
328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     November 10, 2004, 16:36:12; Search time 19.3368 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-092-750-2
US-10-092-750-41
US-09-828-870-35
US-09-828-870-35
US-09-828-870-18
US-09-828-870-18
US-10-101-482-2
US-10-101-482-2
US-10-101-482-9
US-10-101-482-9
US-10-101-482-9
US-10-101-482-9
US-10-101-482-9
US-10-101-482-9
US-10-101-482-9
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US-10-101-482-9
US-10-101-482-9
                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                         US-10-092-750-41
90
1 GQVGRQLAIIGDDINRK 18
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Maximum DB seq length: 200000000
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Match Length DB
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198
198
200
111
2011
2011
2011
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Perfect score:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                             Searched:
                                                                                                       Run on:
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No.
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121109876543121
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17; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-828-870-36
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US-09-828-870-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/236,385
FILING DATE: 25-JANUARY-1999
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-942-840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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LUTZ, Robert J.
TITLE OF INVENTION: WOUNEL PREPIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,870
FILING DATE: 10-APPT-2001
CLASSIFCATION: «URNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                               APPLICANT: Wright, Martin C.

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REPERENCE: 50036/05002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR APPLICATION NUMBER: US 60/274,526

WIMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%; Score 85; DB 11; I
llarity 100.0%; Pred. No. 4.1e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 90; DB 14; 100.0%; Pred. No. 5.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear;

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-828-870-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/09828870 Publication No. US20040054129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GOVGROLAIIGDDINRRK 18
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GOVGROLALIGDDINRRK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 35 SEQUENCE CHARACTERISTICS
APPLICANT: Hammond, Philip W.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                            SEQ ID NO 41
LENGTH: 18
TYPE: PRT
CREANISM: Homo sapiens
US-10-092-750-41
                     Alpin, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-828-870-35
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PRIOR APPLICATION NUMBER: 09/236,385
PILING DATE: 25-JANUARY-1999
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                       APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: WOULL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION NOUSL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Score 85; DB 11; Length 20; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,870
FILING DATE: 10-APP-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-828-870-36; Sequence 36, Application US/09828870; Publication No. US20040054129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09828870 Publication No. US20040054129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GOVGROLAIIGDDINRR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GOVGRQLAIIGDDINRR 17
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                           NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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Length 28;

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Query Match
94.4%; Score 85; DB 11; I
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                       TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-828-870-18
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TELEPAX: 202-942-684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GOVGRQLAIIGDDINRR 17
           INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GOVGROLAIIGDDINRR 22
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APPLICATION NUMBER: 09/236,385

FILING DATE: 25-JANUARY-1999

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
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Sequence 18, Application US/09828870
Sequence 18, Application US/09828870
Publication No. US20040054129A1
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APPOPTOSIS
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828,870

FILING DATE: 10-Apr-2001

CLASSIFICATION: CURKOWD>

PRIOR APPLICATION DATE: 25-JANUARY-1999

ATTORNEY AGENT INFORMATION:

WARTON TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO T
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ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER: LORDY disk
COMPUTER: IBM PC Compatible
OCNFUTER: IBM PC Compatible
OCNFUTER: DATE: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/828,870
FILING DATE: 10-Apr-2001
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-828-870-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%; Score 85;
100.0%; Pred. No.
:ive 0; Mismatcl
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TELEFAX: 202-942-6484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-828-870-18
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FILING DATE: 25-JANUARY-1999
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
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Publication No. US20040054129A1
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TILLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBELE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,870
FILING DATE: 10-Apr-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
Indels
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94.4%; Score 85; DB 11;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
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US-10-101-482-22
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US-10-101-482-7
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US-10-101-482-22
Sequence 22, Application US/10101482
Publication No. US2003008837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
Sequence 0, Application US/10189294
; Publication No. US20030060615A1
; Publication No. US20030060615A1
; GENERAL INPORMATION:
    Gibson, Helen L.
    Fitzpatrick, Paul A.
    Barr, Philip N.
    TITLE OF INVENTION: A NOVEL BAK BINDING PROFEIN, DNA
    ENCODING THE PROTEIN, DNA
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORDY

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/189,294

FILING DATE: 01-Jul-2002

CLASSIFICATION: CURNOWN>

PRIOR APPLICATION OF CURNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/381,488

FILING DATE: 11-Feb-2000

ATTORNEY/AGENT INFORMATION:

NAME: BROWN, THERESA A.

REGISTRATION NUMBER: 32,547

REFERENCE/DOCKET NUMBER: 4147-15-PUS

TELEPHONE: (303) 865-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: /note= "Bak (delta)2 (delta)TM"
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWN, THERESA A.
STREET: 1560 Broadway, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..117
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserv
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Sequence 7, Application US/10101482
Publication No. US20300008837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: KIEFER, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-MAR-2002
CLASSIFICATION NUMBER: US/08/320,157
FILING DATE: OT-CCT-1994
ATTORNEY/ABOTI INFORMATION:
NAME: LEHNHARDT, SUGAN K.
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 33,943
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTEY 103A

ZIP: 94304-11018

COMPUTER READBLE FORM:
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <UNKnown>
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APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 813-560
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GOVGRQLAIIGDDINRR 17
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72 GQVGRQLAIIGDDINRR 88
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US-10-101-482-11
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                                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KIEFER, MICHAEL C.
BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-WODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRING PSTIGNON DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.4%; Score 85; DB 14; Length 21 Best Local Similarity 100.0%; Pred. No. 5.6e-06; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: LEHRHARDY, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 83-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-OCT-1994
                                          TELEX: 7012) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; TANGTH: 211 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-101-482-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-101-482-9
                        TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-101-482-9
; Sequence 9, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 211 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 1 GOVGROLALIGDDINRR 17
                                                                                                                                                                                                                                                                                                                                                                                                   72 GOVGROLAIIGDDINRR 88
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/10101482
Publication No. US20300008837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
BARR, PHILIP J.
TITLE OF INVENTION: BACODING THE PROTEINS AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                   CORRESPONDERS SEQUENCES: 2.2
CORRESPONDER ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentil Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-MAR-2002
CLASSIFICATION AND ATA:
APPLICATION NUMBER: US/00/101,482
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAMM: LEHHWARDF, 203A03
REFERENTION NUMBER: 33,943
REFERENTION NUMBER: 23647-20007.20
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
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100.0%; Pred. No. 5.6e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22
CORRESPENDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 813-5600
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
                                                                                               APPLICANT: KIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 211 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 GOVGROLATIGDDINRR 88
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Best Local Similarity 100.0
Matches 17; Conservative
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94.4%; Score 85;
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Kamatkar, Shubhangi
Mertens, Maureen
Myer, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bast Jr., Robert C.
Hortobagyi, Gabriel N
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GOVGRÓLAIIGDDINRR 88
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-177-293-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-177-293-25
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Gibson, Helen L.
Fitzpatrick, Paul A.
Barr, Philip J.
TITLE OF INVENTION: BAK BINDING PROTEIN, DNA
ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
STATE: Callic....

COUNTRY: USA

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRITOR DATE: 18-Mar-2002

FILING DATE: 18-Mar-2002

CLASSIFICATION NUMBER: US/08/320,157

FILING DATE: UNFOWNATION:
APPLICATION NUMBER: US/08/320,157

FILING DATE: OT/OCT-1994

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,943

REGISTRATION NUMBER: 33,943

FELESPERSION CRET NUMBER: 23647-20007.20

TELEPRANCE/DOCKET NUMBER: 23647-2007.20

TELEPRANCE/DRESS: SIGGE

TYPE: AMINO ACID

SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDE/DRESS: SIGGE

TOPOLOGY: 1=-200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Score 85; DB 14; Length 211; 100.0%; Pred. No. 5.6e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/189,294
FILING DATE: 01-Jul-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWN, THERESA A.
STREET: 1560 Broadway, Suite 1200
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/381,488
FILING DATE: 11.Feb-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10189294; Publication No. US20030060615A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GOVGRQLAIIGDDINRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 GOVGROLAIIGDDINRR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CO
COUNTRY: USA
ZIP: 80202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-101-482-11
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US-10-189-294-2
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APPLICANT: FUBLOAN:
APPLICANT: FUBLOAN
APPLICANT: Sahin, Aysegul
APPLICANT: Sahin, Aysegul
APPLICANT: Main, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFREBANCE: MAI-038
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/305,501
PRIOR FILING DATE: 2001-09-25
PRIOR PRILING DATE: 2001-09-25
PRIOR PRILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NOS: 506
SEQ ID NO 25
FIRMTH: MINDER: FARESEQ FOR Windows Version 4.0
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NAME: BROWN, THERESA A.
REGISTRATION NUMBER: 32,547
REPERRENCE/DOCKET NUMBER: 4147-15-PUS
TELECOMMINICATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (310) 863-9700
TELEPAX: (310) 863-9700
TELEPAX: (310) 863-9700
TENGTH: 211 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
```

DB 14; Length 211;

0; Gaps Best Local Similarity 100.0%; Pred. No. 5.6e-06; Matches 17; Conservative 0; Mismatches 0; Indels

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ò Dp Search completed: November 11, 2004, 01:28:23 Job time : 20.3868 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 4.01036 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-41 90 1 GQVGRQLAIIGDDINRRK 18 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Bak protein - huma	-2 protein	protein phosphatas	H+/K+-exchanging A	probable copper-tr	probable ATPase yb	Ču(I)-translocatio	cation transport A	F54F2.1 protein -	doc	enolase - Helicoba	phytoene dehydrode	IS66 family Orf4 (	sy v-atpase proteo	probable chemorece	prot	tran	pilus biogenesis p	copper-t	probable protein p	probable transcrip	response regulator	`		phosphopyruvate hy	probable enolase [	oxidoreductase [im	й	_
SUMMARIES	ID	887	œ	0	AE0564	C64779	E85546	A90696	H82104	S44824	S58684	H71967	JN0084	AC3205	H75027	B71213	T48031	875352	G82618	E70041	H84643	G71906	G64607	JQ1185	in	$\sim$	8694	E90316	m	2399
	DB	. 2	~	N	~1	Н	N	7	N	N	N	~	7	7	~	~	7	~	N	Н	Ω	~1	N	~	~	~	N	7	7	7
	Length	211	М	357	m	m	E	834	Н	N	$\alpha$	N	3	m	S	φ	7	O)	693	0	S	æ	æ	4	4	446	4	S	664	r-
ok ok	Query Match		4	51.7	51.1	Η.	Η.	ä	ä	ä	ö	ö	σ.	æ	œ	œ	œ	æ.	48.9	œ.	φ.	ζ.	7.	۲.	۲.					
	Score	85	85	46.5	46	46	46	46	46	46	45	45	44.5	44	44	44	44	44	44	4	43.5	43	43	43	43	43	43	43	43	43
	Result No.	7	N	m	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

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Gaps

.. 0

0; Indels

ઠ g RESULT 2 S58875

cdn-2 protein - human C;Species: Homo sapiens (man) C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

probable H+/K+-exc	ribose-phosphate d	ribose-phosphate d	catalase (EC 1.11.	cell division prot	cell division prot	cu2+-exporting ATP	hypothetical prote	crossover junction	crossover junction	Holliday junction	chemotaxis protein	hypothetical prote	probable minor cap	methyl-accepting c	methyl-accepting c
B95969	S71460	A53433	860757	D97708	C71712	D95330	H7.1313	A85799	D38113	E90950	T44678	S67451	T13091	C72291	F72288
7	ď	~	~	(1	N	N	~	N	ď	N	N	N	N	N	01
827	356	356	482	637	637	826	70	173	173	173	251	329	447	530	539
47.8	46.7	46.7	46.7	46.7	46.7	46.7	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.6
43	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Bak protein - human

NiAlternate names: bcl-2 homolog; cdn-1 protein

C; Species: Homo sapiens (man)

C; Accession: S58873; S58874

R; Chittenden, T; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I., R; Chitten and T. A.; The sapient of apoptosis by the Bcl-2 homologue Bak.

A; Reference number: S58873; MUID: 95231653; PMID: 7715730

A; Recession: S58873; MUID: 95231653; PMID: 7715730

A; Residues: Dreliminary; nucleic acid sequence not shown

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-21 CCHI.

A; Residues: 1-21 CCHI.

A; Residues: 1-21 CCHI.

A; Residues: 1-21 CCHI.

A; Cross-references: UNIRROT: 016611; EMBL: U23765; NID: 975879; PIDN: AAA933066.1; PID: 975875

R; Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martinc, N; Reference number: S58872; MUID: 95231652; PMID: 7715729

A; Reference number: S58872; MUID: 95231652; PMID: 7715729

A; Reference number: S58872; MUID: 95231652; PMID: 7715729

A; Reference number: S58872; MUID: 95231652; PMID: 7715729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Colecule type: mRNA
A;Cross-references: EMBL:X84213; NID:g804984; PIDN:CAA58997.1; PID:g804985
B;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, J.
A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A;Accession: S58874; MUD:95231654; PMID:7715731
A;Accession: S58874
A;Status: preliminary
A;Accession: S58874
A;Status: preliminary
A;Accession: S58874
A;Residues: 1-21 <KIB>
A;Cross-references: EMBL:U16811; NID:g595923; PIDN:AAA74466.1; PID:g595924
A;Gene:ion: GDB:BAK
A;Gene: GDB:BAK
A;Gene: GDB:BAK
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Pred. No. 1.2e-06;
0; Mismatches 0;
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Best Local Similarity 100.0%; P

Matches 17; Conservative 0;
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Length 211;

94.4%; Score 85; DB 2; Length 211 100.0%; Pred. No. 1.2e-06; ive 0; Mismatches 0; Indels

ilarity 100.0%; Pi Conservative 0;

Best\_Local Similarity Matches 17; Conserv

Query Match

72 GQVGRQLAIIGDDINRR 88

1 GOVGRQLAIIGDDINRR 17

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C.Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bindi C.Superfamily: Bacillus probable copper-transport; metal binding; phosphoprotein; F.9-38(Domain: heavy-metal-associated homology <htbody>
F.9-38(Domain: heavy-metal-associated homology <htbody>
F.108-134/Domain: heavy-metal-associated homology <htbody>
F.108-24/Domain: transmembrane #status predicted F.108-134/Domain: transmembrane #status predicted F.224-568/Domain: transmembrane #status predicted F.238-454/Domain: transmembrane #status predicted F.348-454/Domain: transmembrane #status predicted F.348-454/Domain: transmembrane #status predicted F.348-454/Domain: transmembrane #status predicted F.349-454/Domain: transmembrane #status predicted F.349-454/Domain: transmembrane #status predicted F.349-454/Domain: transmembrane #status predicted F.349-454/Domain: transmembrane #status predicted F.349-785/Domain: transmembrane #status predicted F.353/Active site: Asp (aspartylphosphate intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cjaccession: C64779
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucceic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosaiduse; 1-834 SBLATA
A;Cross-references: UNIRKOT:059385; GB:AE000154; GB:U00096; NID:g1786683; PIDN:AAC73586.1
A;Experimental source: strain K-12; substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable Arpase ybaR [imported] - Escherichia coli (strain O157:H7, substrain EDL933) C;Species: Escherichia coli (cjoate: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: EB5546 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Nature 409, 529-533, 2001 Aritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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A,Residues 1.834 «STO»
A,Cross-references: UNIPROT:08XD24; GB.AE005174; NID:g12513357; PIDN:AAG54833.1; GSPDB:GP
A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable copper-transporting ATPase (EC 3.6.1.-) - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Os-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
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Pred. No. 19;
3; Mismatches 1; Indels
                                                                                Length 833,
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                                                                                                                                                                                          Mismatches
                                                                                               Score 46;
Pred. No.
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66.7%;
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66.7%;
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712 GRQVAMVGDGIN 723
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711 GRQVAMVGDGIN 722
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Matches 8; Conservative
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C; Keywords: hydrolase
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A,Gene: ybaR
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C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind
C;Accession: S58875
R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, Mature 374, 736-739, 1995
A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A;Reference number: S58875
A;Accession: S58875
A;Accession: S58875
A;Status: perliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-211 cKIE>
A;Residues: 1-211 cKIE>
A;Cross-references: UMIPROT: Q13014; EMBL: U16812; NID: 9595925; PIDN: AAA74467.1; PID: 959593 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
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R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; I ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A;Reference number: 215589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T06308
A;Molecule type: DNA
A;Residues: 1-37 <BEV>
A;Fesidues: 1-37 <BEV>
A;Cross-references: UNIPROT:Q9SZS3; EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60
A;Experimental source: cultivar Columbia; BAC clone F11C18
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
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A:Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C:Superfamily: human phosphoprotein phosphatase 1A
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Length 357;

DB 2;

Score 46.5; DB Pred. No. 6; 4; Mismatches

51.7%; 58.8%;

Query Match
Best Local Similarity 58.8
Matches 10; Conservative

A; Gene: ATSP: F11C18.60

4

104 GQRGWRELAVLGDKINK 120

Genetics:

GOVG-ROLAIIGDDINR 16

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Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Substance names: enolase C. Adcession: Helicobacter Pyloxi C. Date: 29-Nov-1995 #Sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 C. Adcession: B64539; SS6684 Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary Subsidiary 
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C;Function:
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosp
A;Pathway: glycolysis
G;Superfamily: enolase
C;Superfamily: enolase
C;Skeywords: carbon-oxygen lyase; gluconeoqenesis; glycolysis: hydro-lyase: magnesium
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                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                         RiAnderson, K.

Submitted to the EMBL Data Library, September 1993
A; Description: Sequence of the C. elegans cosmid F54F2,
A; Reference number: 844817
A; Accession: 844817
A; Accession: 844812
A; Accession: 844812
A; Accession: 84482
A; Accession: 84812
A; Accession: 84812
A; Accession: 84812
A; Accession: 84812
A; Cross-references: UNIPROT: P34446; EMBL: L23645; NID: 9388603; PID: 9388605
C; Genetics:
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Pred. No. 13;
6; Mismatches
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Pred. No. 29;
4; Mismatches
                                                                                                   F54F2.1 protein - Caenorhabditis elegans
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Best Local Similarity 53.8%;
Matches 7; Conservative
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A;Residues: 1-25,'I',27-68 <SCH>
A;Cross-references: EMBL:235478
C;Genetics:
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Best Local Similarity
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A90696
Cu(17)
A90696
Cu(17)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Reference number: A99629; MUDD:21156231; PMID:11258796
A;Accession: A90696
A;Accession: A90696
A;Accession: A90696
A;Residues: 1-834 <HAY>
A;Residues: UNIPROT:Q8XD24; GB:BA000007; PIDN:BAB33960.1; PID:g13359994; GSPDB:GCGenetics:
A;Genetics:
A;G
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H82104

cation transport ATPase, B1-E2 family VC2215 [imported] - Vibrio cholerae (strain N16961)
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Ju1-2004
C; Accession: H83104
R; Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. A; Tele: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-915 <HB2
A; Residues: 1-915 <HB2
A; Residues: 1-915 <HB2
A; Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C; Genericae:
A; Gene: VC2215
A; Map position: 1
C; Suberfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind
C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind
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Pred. No. 19;
3; Mismatches 1; Indels
                                                                                          2; Length 834;
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Larity 64.3%; Pred. No. 21;
Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                 Indels
                                                                                      Score 46; DB 2
Pred. No. 19;
3; Mismatches
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ilarity 66.78;
Conservative
                                                                                      51.1%;
66.7%;
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712 GRQVAMVGDGIN 723
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712 GRQVAMVGDGIN 723
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Matches 8; Conserv
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Matches 8; Conserv
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probable chemoreceptor protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: B1213
R;Rawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Sekine
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi,
DNA Res: 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an
A;Reference number: A71000; MUID:98344137; PMID:9679194
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross_references: UNIPROT:Q8UJV6; GB:AE008687; PIDN:AAL46057.1; PID:g17743817; GSPDB:GA;Experimental source: strain C58 (Dupont)
C;Genetics:
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A;Residues: 1728 <KAW>
A;Cross-references: UNIPROT:Q9UXV1; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50662
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1189
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                 ster, E.W.
AyTitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC3205
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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red. No. 9.9;
Mismatches 3
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Pred. No. 11;
4; Mismatches
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Pred. No.
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GEAGRGFAVVADEIRR 137
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Best Local Similarity 43.0%
The Conservative
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Matches 7; Conser
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A; Residues: 1-234 < KUR>
                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Genome: plasmid
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC3205 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
R;Wood, D;W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                 C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Ccession: H71967
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature 397, 176-180, 1999
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MuID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
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C;Molecule                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JN0084
R;Schmidt, A.; Sandmann, G.
Rene 91, 113-117, 1990
A;Title: Cloning and nucleotide sequence of the crtl gene encoding phytoene dehydrogenas A;Reference number: JN0084; MUID:90382685; PMID:2119326
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A;Reaidues: 1-532 «GN-521 (GN-M55647; GB:M33237; NID:g141989; PIDN:AAA62573.1;
A;Cross-references: UNIPROT:P21134; GB:M55647; GB:M33237; NID:g141989; PIDN:AAA62573.1;
A;Note: the authors translated the codon CAG for residue 380 as Gly
C;Comment: This enzyme catalyzes the symmetrical introduction of two double bonds at C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS66 family Orf4 (truncated) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Aphanocapsa phytoene dehydrogenase
C;Superfamily: Aphanocapsa phytoene dehydrogenase
C;Superfamily: Aphanocapsa phytoene dehydrogenase
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6; Mismatches
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Pred. No.
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Query Match

48.9%; Score 44; DB 2; Length 261;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 5; Indels
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Search completed: November 10, 2004, 13:40:49 Job time: 5.01036 secs

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GenCore version 5.1.6

Copyright (c) 1933 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 12:27:34; Search time 21.9793 Seconds

(without alignments)

471.205 Million cell updates/sec
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Title:
US-10-092-750-41
Perfect score: 90
Sequence: 1 GQVGRQLAIIGDDINRRK 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_02:\*
 1: uniprot\_sprot:\*
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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% Query Match	94.4	94.4	94.4	94.4	94.4	93.3	92.2		92.2	92.2	92.2	54.4	52.2	51.7	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1		51.1	50.6	ö	50.0	•	50.0
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94.4%; Score 85; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 9.9e-06;

Matches 17; Conservative 0; Mismatches 0; Indels

 Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TAXID=9606;

[1] -SEQUENCE FROM N.A. Ma J.;

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ENO HELPJ ENO_HELPJ C82CN7 C82CN7 C6CFX2 C8UV46 C9UXV1 C57733 C7332 C7332 C72837 AAS96278 C72837 AAS96278 C735C2 C915C2	ALIGNMENTS	PRT; 80 AA. Created) Last sequence update) Last annotation update)	Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae; Cetartiodactyla; Suina; Suidae; to the EMBL/GenBank/DDBJ datab 4598.1; BG12_BH. BG12_BH. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
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Fri Nov 12 14:55:25 2004

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SEQUENCE FROM N.A. REDMED-7715731; Wu J.J., Umansky S.R., Kiefer M.C., Barre M.J., Powers V.C., Wu J.J., Umansky S.R., Tomei L.D., Barr P.J.; "Modulation of apoptosis by the widely distributed Bcl-2 homologue 05-JUL-2004 (Rel. 44, Last annotation update) Putative Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update PRT; Name=BCL2L7P1; Synonyms=BAK2; Homo sapiens (Human). 

Nature 374:736-739(1995).

-!- FUNCTION: In the presence of an appropriate stimulus, accelerates programmed cell death by binding to, and antagonizing the a repressor Bcl-2 or its adenovirus homolog BIB 19k protein.

-!- SUBUNIT: Forms heterodimers with Bcl-2, EIB 19k protein, and Bcl-

1. SUBCELLULAR LOCATION: Membrane-associated (Potential).

1. TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with highest levels in the heart and skeletal muscle.

1. DOMAIN: Intact BH3 domain is activity and for their interaction with anti-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

2. SIMILARITY: Belongs to the Bcl-2 family. Apoptotic members of the Bcl-2 family.

3. SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

4. SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

5. CAUTION: This is probably the product of a pseudogene.

7. CAUTION: This is probably the product of through a collaboration between the Swiss Institute of Bolinformatics and the EMB1 outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch).

EMBL; U16812; AAA74467.1; -. PIR; S58875; S58875.

Potential. 703875EC4DCCC1D3 CRC64; HSSP, Q16611, 1BXL.

Genew, HGNC:996; BGL2L7P1.

GO; GO:0016020; Cimembrane; NAS.

GO; GO:0006917; P:induction of apoptosis; NAS.

InterPro; IPR00712; Bcl2 BH.

InterPro; IPR00712; Bcl2 EH.

InterPro; IPR00712; Bcl2 II.

PROSTITE; PS500654; BCL2 II.

PROSTITE; PS500659; BCL2 II.

PROSTITE; PS01080; BH1; II.

PROSTITE; PS01080; BH2; II.

PROSTITE; PS01289; BH2; II.

PROSTITE; PS01289; BH3; II.

Apoptosis; Hypothetical protein; Transmembrane.

DOMAIN 117 136 BH1. BHZ. 23411 MW; 211 AA; 169 188 DOMAIN TRANSMEM SEQUENCE REPERMENTAL SOLUTION OF THE SOLUTION OF THE PROPERTY OF THE PR

Gaps .. 0 Length 211; Score 85; DB 1; Le Pred. No. 2.6e-05; Mismatches 94.4%; SCC... 100.0%; Pre/ 0; h Local Similarity 100. es 17; Conservative Query Match Matches

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BAK HUMAN STANDARD; PRT; 211 AA.
Q16611; Q92533;
Q1.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
BC1-2 homologous antagonist/killer (Apoptosis regulator BAK) (BCL2like 7 protein)

Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Name=BAK1; Synonyms=BAK, BCL2L7;

TISSUE=B-cell;
MEDLINE=95231652; PubMed=7715729;
Barrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,
Grinham C.J., Martinou J.C., Brown R.;
"Cloning of a bcl-2 homologue by interaction with adenovirus EIB SEQUENCE FROM N.A. NCBI TaxID=9606;

Nature 374:731-733(1995). SEQUENCE FROM N.A.

MEDLINE-95231653; PubMed-7715730; Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J., Evan G.I., Guild B.C.; "Induction of apoptosis by the Bcl-2 homologue Bak."; Nature 374:733-736(1995)

'Modulation of apoptosis by the widely distributed Bcl-2 homologue SEQUENCE FROM N.A. MEDLINE=99231654; PubMed=7715731; Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R., Tomei L.D., Barr P.J.; Nature 374:736-739(1995).

Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; WIERS-SYRS, environmental genome project, NIERS ESIS478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; 

Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J., Elangovan B., Chinnadurai G., Lutz R.J.; "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell death and protein binding functions."; EMBO J. 14:5589-5596(1995).

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Query Match
MEDINE-ZURSES; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-ZURSES; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.P., Zeeberg B. B., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwar P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaibb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaibbs R.A.,

Rahesley R.W., Touchman M., Madan A., Sodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Warsha M.A., Schell H. H. Wanner M.A.,

Butterfield Y.S.N., Warsha M.A.,

Butterfield Y.S.N., Warsha M.A.,

Butterfield Y.S.N., Warsha M.A.,

Butterfield Y.S.N., Warsha
                                                                         REMEDIANCE FROM N.A.

REMOLINEE-2935763; PubMed=14574404; DOI=10.1038/nature02055; RA BEDLINEE-2935763; PubMed=14574404; DOI=10.1038/nature02055; RA MINITES E. Scott C.E.

RA Almed a J.P. Ambrose M.C., Horton R. Hunt S.E., Scott C.E.

Almed a J.P. Ambrose K.D., Bathel G., Milne S., AlmeGough R., Bachel G., Milne S., AlmeGough R., Bachel G., Milne S., AlmeGough R., Barbage A.K., Bagguley C.L., Bailey T., Banearjee R., Barker D.J., Barlow K.F., Barguley C.L., Bailey H. Beasley O., Bird C.P., Barroth J. Carder G., Carter N.P., Blarker D.G., Burrill W., Burton J., Carder G., Carter N.P., Burford D.C., Clark S.Y., Clark G., Clee C.M., Cleeg S., Cobley V., Burner D.G., Colmen L.K., Corly N.R., Coville G.J., Collier R.E., Drankland J.French L., Garner P., Garner D., Harly L.M., Gillson C.J., Glitcher B.J., Howell S.M.D., Frankland J. Frankland D., Gillson C.J., Glitcher B.J., Howell G.K., Howle B. A., Arankland J.F., Harle E.A., Haath P.D., Heathcott R., Hombris S.J., Howden D.J., Howell G.K., Howle B., Holmes S.J., Howden D.J., Howell G.K., Howle B., Holmes S.J., Howden D.J., Howell G.K., Howle B., Holmes S.J., Howden D.J., Howell G.K., Howle B. M., Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Loyd C.R., Nobercon T., Moreland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M., Moreland J.E., Lovell J., Martin S., Maire M., Mohammadi M., Moreland J.E., Lovell J., Martin S., Maire M., Ross M.T., Searle S.M., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Ramesy Y., Rame
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
MEDLINE=96091131; PubMed=8521816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 96-206 FROM N.A.
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                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                Programmed cell death by binding to, and antagonizing the a programmed cell death by binding to, and antagonizing the a repressor Bcl-2 or its adenovirus homolog BlB 19k protein.
                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- INSUB SPECIFICITY: Expressed in a wide variety of tissues, with highest levels in the heart and skeletal muscle.
-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and BAK for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
-!- SIMILARITY: Conteains 1 Bcl-2 family.
-!- SIMILARITY: Conteains 1 Bcl-2 homology 2 (BH2) domain.
-!- SIMILARITY: Conteains 1 Bcl-2 homology 3 (BH3) domain.
STRUCTURE BY NWR OF 72-87.

MEDLINE=97172562; PubMed=9020082;
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
Sattler M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.,
Thompson C.B., Fesik S.W.;
Structure of BRI-XL-Bak peptide complex: recognition between
regulators of apoptosis.";
Science 275:983-986(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIK; $58873; $58873.

PDB; 1BXL; NWR; B=72-87.

Genew; HGNC; 9-9; BAK1.

MIM; 600516; 9-9

GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.

InterPro; IPR000712; Bcl2 BH.

InterPro; IPR02475; BcL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
23409 MW; A2200FE72A46D04E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; Polymorphism; Transmembrane.
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/FTId=VAR_018829.
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/FTId=VAR_018830
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EMBL, U23765; AA493066.1; -.
EMBL, U16811; AAA74466.1; -.
EMBL, AX260471; AAA744628.1; -.
EMBL, ES004431; AAA44431.1; -.
EMBL, D88397; BAA13606.1; -.
EMBL, D88397; BAA13606.1; -.
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188
28
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DB 1; Length 211;

94.4%; Score 85;

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Gaps

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Indels

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Mismatches

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16; Conservative
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Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

"Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR.201).",

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR457419; CAG33700.1; -.

SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                        Gaps
                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Ovary;
Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF164518; AAR89533.1; -
GO; GO:0042981; P:regulation of apoptosis; IEA.
InterPro; IPR000712; Bc12_BH.
InterPro; IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                                                                                                                                           01-UUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Bak protein (Fragment).
          Pred. No. 2.6e-05;
; Mismatches 0;
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100.0%; Pred. No. 2.6e-05;
ive 0; Mismatches 0;
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94.1%; Pred. No. 2.9e-05;
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SMART; SM00337; BCL; 1.
PROSITE; PS01060; BRL2 TAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
100.0%; F1.
                                            1 GOVGRQLAIIGDDINRR 17
                                                               72 GOVGROLAIIGDDINRR 88
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Matches 17; Conservative
                    17; Conservative
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Matches 17; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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CAG33700;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Neuronal;
SURAIN=2123330; PubMed=11278671;
Sun Y.F., Yu L.Y., Saarma M., Timmusk T., Arumae U.;
Sun Y.F., Yu L.Y., Saarma M., Timmusk T., Arumae U.;
"Neuron-specific Bcl-2 homology 3 domain-only splice variant of Bak is
"Neuron-specific Bcl-2 homology 3 domain-only splice variant of Bak is
anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.";
J. Biol. Chem. 276:16240-16247(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Straubberg R.;
Submitted (SEP-2003) to the EWEL/GenBank/DDBJ databases.
EMBL; AF402617; AALO1876.1;
EMBL; AF402617; AALO1876.1;
EMBL; PC57589; AAH57589.1;
MGP; MGI:1097161; Bakl.
GO; GO:0006652; P:caspase activation via cytochrome c; IMP.
InterPro; IPR002712; BC12 BH.
InterPro; IPR002715; BC12-family.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
N-BAX1.
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                                                                                                                                                                                                                                                                                                               151 AA
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PROSITE; PS50062; BCL2; PAMILY; 1.
PROSITE; PS01259; BH3; 1.
SEQUENCE 151 AA; 16402 NW; 18
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    17
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                     31 GOVGROLAVIGDDINRR
1 GOVGROLAIIGDDINRR
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Matches 16; Conserv
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STRAIN=Swiss; TISSUE=Liver;
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       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINELS238255; PubMed=1247932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Loddin T.B., Bonaldo M.F., Casavant T.L., Scheezz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raheeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

A Hakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCDI_TaxID=10090;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057589; AAH57589.1; -.
SEQUENCE 151 AA; 16402 MW; 18C13BFF86E4F33B CRC64;
                                                                                                                                                                                                                                         AAH57899 PRELIMINARY; PRT; 151 AA.
02-MAH-27089 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Baki protein.
Mus musculus (Mouse)
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                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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GOVGROLAIIGDDINRR 17
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Matches 16; Conserva
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SEQUENCE FROM N.A.
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Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-
length enriched library, clone:F630041023 product:BCL2-
antagonist/killer 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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InterPro; IPR000712; Bc12_BH.
InterPro; IPR002475; BC12_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 1; Length 208;
Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 BH3.
133 BH1.
181 BH2.
202 Potential.
23300 MW, DAFC11B160C523C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; BC1-2; 1. —
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH3; 1.
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HSSP; Q16611; 1BXL.
MGD; MGI:1097161; Bak1.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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166 1
185 2
208 AA;
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                                                                                                                                                                 similarity),
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Q8C264;
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Best Local 6, Conservative
Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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01-OCT-2000 (
01-MAR-2004 (
                                                                                                                                                                                                                                 BAK protein.
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ID K6P3_BACTN
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                                                                                                                           RESULT 11
Q9JK59
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B. Submitted (ARP-2002) to the EMBL/GenBank/DDBJ databases.

B. MGD, MGI:1097161; Baki.

B. MGD, MGI:1097161; Baki.

B. HirerPro; IPRO0712; Bc12 BH:

B. HirerPro; IPRO0712; Bc12 BH:

B. HirerPro; IPRO0712; Bc12 Emily.
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata K., Itoh M., Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                           ĕ
                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-673(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watsunki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                          RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23234 MW; 55E72D29A8AAFD18 CRC64;
                                                         Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                STRAIN=NOD;
MEDLINE=21085660; PubMed=11217851;
                                           MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGRI, PF00452; BG1-2; 1.
SWART; SM00337; BCL; 1.
PROSITE; PS01062; BCL2 FAMILY; 1.
PROSITE; PS010259; BH2; 1.
PROSITE; PS010259; BH3; 1.
SEQUENCE 209 AA; 23234 MW; 551
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The FANTOM Consortium,
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12653928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley,
MEDLINE=22672518; PubMed=12787069;
ILCh T., Itch A., Pleasure D.;
"BCl-2-related protein family gene expression during oligodendroglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                               Gaps
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Bacteroides thetalotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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10-0CT-2003 (Rel. 42, Last sequence update)
10-5UL-2004 (Rel. 44, Last annotation update)
6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase (Phosphohexokinase 3).
Score 83; DB 2; Length 209;
Pred. No. 5.4e-05;
1; Mismatches 0; Indels
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Pred. No. 5.4e-05;
1; Mismatches 0; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.";
d. Neurochem. 85:1500-1512(2003).
EMBL; AF259510.1;
HSSP; O16611; 1BXL.
GO: GO:0042981; P:regulation of apoptosis; IEA.
InterPro; IPR0004712; BCL2_EM11Y.
InterPro; IPR000475; BCL2_family.
Ffam; PF00452; BCL2_i.
SMART; SM00337; BCL2_i.
PROSTIE; PS01080; BH1; UNKNOWN_1.
PROSTIE; PS01289; BH2; 1.
PROSTIE; PS01289; BH2; 1.
PROSTIE; PS01289; BH2; 1.
PROSTIE; PS01289; BH2; 1.
PROSTIE; PS01289; BH2; 1.
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PROSTIE; PS01289; BH2; 1.
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Query Match
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Matches
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             RAT REA DE DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE COR DE CO
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                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license also remember (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=306 / ATCC 13902 / XV 101;

XX MEDINEE-22022145; PubMed=12024217;

Ad Silva A.C.R.; Ferro J.A.; Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Couttinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kibin L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Amarins E.C., Machado M.A., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

Amarins E.C., Machado M.A., Nenck C.F.M., Miyaki C.Y., Moon D.H.,

Amarins E.C., Machadia J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Amarins E.C., Machado M.A., Sena J.A.D., Silva C., de Souza R.F.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P06999; 2PFK.
HAMAP; MF 00339; -; 1.
InterPro! IPR000023; Ppfruckinase.
Pfam; PF00365; PFK, 1.
PRINTS; PR00476; PHFRCTKINASE.
ProDom; PD00070; Ppfruckinase; 1.
PROSITE; PS00433; PHOSPHOFRUCYKINASE; FALSE NEG.
Allosteric enzyme; ATF-binding; Complete proteome; Glycolysis; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
-!- PATHWAY: Key control step of glycolysis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphofructokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
W, 990BAEFGESEDSF79 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hemagglutinin/Demolysin-related protein.
OrderedLocusNames=XAC1816;
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NCBI_TaxID=92829;
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      299:2074-2076 (2003).
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336 AA;
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les 9; Conserv
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Magnesium;
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Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
Nature 417:459-463(2002).
BMBL, AAMSON S. AAMSON S. Fil heemagg.
PF005594; Fil heemagg.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Condera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Souliwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Hoheisel J., Mewes H.W.
Lemcke K., Mayer K.F.X.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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52.9%; Pred. No. 2.2e+02;
ive 2; Mismatches 6; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein phosphatase 2C-like protein (AT4931860/FILC18_60).
Name=AT4931860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
Truffi D., Tsai S.M., White F.F.
                                                                                                                                                                                                                                                                                                                                       1430 AA; 145025 MW; 6BA2BCD1BE27E053 CRC64;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel, 13, Last esm
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es 9; Conservative
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STRAINE-VDI-5862 / ATCC 29148;
MEDLINE-22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
science 299:2074-2076(2003).
BMBL, ABO16926, AAO7523821;
Complete protecome; Hypotherical protein.
SEQUENCE 419 AA; 48881 MW; D509382A1524C387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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Bacteroides thetaiotronant.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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Best Local Similarity 50.0%; Pred. No. 91;
Matches 7; Conservative 6; Mismatches 1; Indels
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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58.8%; Pred. No. 65;
tive 4; Mismatches
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Best Local Similarity 58.85
Matches 10; Conservative
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DT 01-JUN-2
DT 01-JUN-2
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Search completed: November 10, 2004, 13:38:48 Job time: 23.9793 secs

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OTHER INFORMATION: 5' 74 amino acids from A. thaliana FAEI (SEQ OTHER INFORMATION: NO:2) and 3' 431 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09877476

Patent No. 6713664

GRERAL INFORMATION:

APPLICANT: Jaworski, Jan G.

APPLICANT: Jaworski, Jan G.

APPLICANT: Jaworski, Jan G.

APPLICANT: Jaworski, Jan G.

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: STATHAGE POLYPEPTIDES

FILE REFERENCE: 07148-108001

CURRENT APPLICATION NUMBER: US/09/877,476

CURRENT APPLICATION NUMBER: US/09/877,476

CURRENT FILING DATE: 2010-06-08

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 505

TYPE: RRT

ORGANISM: Artificial Sequence
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; Patent No. 6713664
; General INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TILLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA; TILLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA; TILLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA; TILLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-08
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-877-476-10
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US-09-877-476-18
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                                                                                                                       November 10, 2004, 12:32:37; Search time 8.981 Seconds (without alignments) 191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lssued_Patents_AA:*
1: /cgTu2_6/ptodata1/iaa/SA_COMB.pep:*
2: /cgTu2_6/ptodata1/iaa/SB_COMB.pep:*
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5: /cgTu2_6/ptodata1/iaa/6B_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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123
1 GVSEAEGTFPLSTFLLGIASRLRSVA 26
                                                                                                                                                                                                                                                                                                                                                                     478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Perfect score:
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4; Length 505; 3; Indels

Score 47; DB 4 Pred. No. 19; 1; Mismatches

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Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-877-476:2
                                                                                                                                                                  RESULT 4
US-09-362-633-2
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                                                           TYPE: PRT ORGANISM: Artificial Sequence FREATURE:
PREATURE:
OTHER INFORMATION: 5' 74 amino acids from A. thaliana FAEI (SEQ ID OTHER INFORMATION: NO.2) and 3' 431 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO.4) having a mutation at CHER INFORMATION: residue 306; designated At74 G306D; hypothetical US-09-877-476-18
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                    Length 505;
                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid sequence of FAE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/88,998
FILING DATE: 0'-JUL 1997
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/329,603
ATTORNEY/AGENT INPORMATION:
NAME: Bactian, Kevin L.

REGISTRATION NUMBER: 34,774
REFERENCE/POCKET NUMBER: 12176-004300
TELECOMMULCATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08888998
Patent No. 6124524
GENERAL INFORMATION
APPLICANT: 11M, Eda
APPLICANT: LIM, Eda
APPLICANT: LIM, Eda
APPLICANT: Hugo K.
ITILE OF INVENTION: FAEI GENES AND THEIR USES
                                                                                                                                                                                                                                                 Score 47; DB 4;
Pred. No. 19;
1; Mismatches
    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18 LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                     9 FPLSTFLLGIASRL 22
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..506
CTHER INFORMATION:
COTHER INFORMATION:
US-08-888-998-2
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                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                   Sequence 2. Application US/09362633
Patent No. 6184355
Patent No. 6184355
GENERAL INFORMATION:
APPLICANT: LIM Eda
APPLICANT: LIM Eda
APPLICANT: MALLER, Janis
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APPLICANT: MALLER, Janis
APPLICANT: MALLER, Janis
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Cr
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Pred. No. 19;
1; Mismatches
Pred. No. 19;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,998
FILING DATE: NUMBER: 08/888,998
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543.9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09877476
Patent No. 6713664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide.
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71.4%;
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 506 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                          9 FPLSTFLLGIASRL 22
                                                                                                23 řPĽTAFĽAGKÁSŘĽ 36
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LENGTH: 506 amino acio
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LOCATION: 1..506
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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FILE REFERENCE: 07148-108001

CURRENT APPLICATION NUMBER: US/09/877,476

CURRENT FILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-06-08

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: PRECED TO WAS: 56

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID OTHER INFORMATION: 5' 114 amino acids from B. napus

OTHER INFORMATION: residues 91 and 92; designated At114 L91C K92R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID
OTHER INFORMATION: 5' 114 amino acids from B. napus
OTHER INFORMATION: elongase KCS (SEQ ID NO:4), having a mutation at
OTHER INFORMATION: position 92; designated At114 K92R
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Pred. No. 19;
1; Mismatches 3; Indels
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38.2%; Score 47; DB

Best Local Similarity 71.4%; Pred. No. 19;

Matches 10; Conservative 1; Mismatches
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Best Local Similarity 71.4%;
Matches 10; Conservative
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LOCATION: (0)...(0)

OTHER INFORMATION: Xaa = Ala or Thr

OTHER INFORMATION: 5' 114 amino acids from A. thaliana FABI (SEQ ID

OTHER INFORMATION: No.2) and 3' 392 amino acids from B. napus

OTHER INFORMATION: elongase KCS (SEQ ID No.4); designated At114
US-09-877-476-8
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38.2%; Score 47; DB 4; Length 506;
Best Local Similarity 71.4%; Pred, No. 19;
Matches 10; Conservative 1; Mismatches 3; Indels
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; Patent No. 6713664
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07146-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
  APPLICANT: Jaworski, Jan G.
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
TITLE OF INVENTION: SYMTHASE POLYBEPTIDES
FILE REFERENCE: 01148-10801
CURRENT APPLICATION NUMBER: US 60/210,326
PRIOR APPLICATION NUMBER: US 60/210,326
PRIOR PLING DATE: 2000-06-08
PRIOR PLING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTERO for Windows Version 4.0
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Batent No. 6713664

GENERAL INFORMATION:
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 506
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; ORGANISM: Arabidopsis thaliana
US-09-877-476-2
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US-09-877-476-12
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LENGTH: 506
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FEATURE:
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAE1 (SEQ ID OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having mutations at OTHER INFORMATION: positions 92 and 307; designated At114 K92R G307D; OTHER INFORMATION: hypothetical
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OTHER INFORMATION: 5' 254 amino acids from A. thaliana FAEI (SEQ ID
OTHER INFORMATION: NO.2) and 3' 252 amino acids from B. napus
OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At254
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Patent No. 671364
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Patent No. 6713664

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jaworski, Jan G.
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COATILE REPRENCE: O7148-108001
CURRENT APPLICATION NUMBER: US/09/877,476
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CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT FILING DATE: 2011-06-08
FRICA APPLICATION NUMBER: US 60/210,326
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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LENGTH: 506
TYPE: PRT
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US-09-877-476-24
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LENGTH: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having mutations at OTHER INFORMATION: positions 91, 92 and 307; designated Atil4 L91C US-09-877-476-20
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38.2%; Score 47; DB 4; Length 506;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 3; Indels
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APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID BLONGASE 3-KETOACYL COATITLE OF INVENTION: SYNTHASE POLYPEPTIDES
FILE REFERENCE: 07148-108001
CURRENT APPLICATION NUMBER: US/99/877,476
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-06-08
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APPLICANT: Jaworski, Jan G.
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
FILE REFERENCE: 07148-108001
    CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,326
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 506
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; Patent No. 6713664
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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US-09-877-476-20
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US-09-877-476-22
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LENGTH: 506
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                                                                                                                                                                                                                               CTHER INFORMATION: 5' 173 amino acids from A. thaliana FAEI (SEQ ID CTHER INFORMATION: NO:2) and 3' 333 amino acids from B. napus CTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated Atl73 NAMEY/KEY: VARIANT IOCATION: (0)...(0) CTHER INFORMATION: Xaa = Pro or Gln US-09-877-476-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
COTHER INFORMATION: 5' 399 amino acids from A. thaliana FABI (SEQ ID OTHER INFORMATION: 0') and 3' 107 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399 NAME/KEY: VARIANT
I LOCATION: (0)...(0)
COTHER INFORMATION: Xaa = Pro or Gln
US-09-877-476-30
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 4; Length 506;
Pred. No. 19;
1; Mismatches 3; Indels
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US-09-877-476-30

Sequence 30, Application US/09877476

Patent No. 6713664

GENERAL INFORMATION:

APPLICANT: Jaworski, Jan G.

TITLE OF INVENTION: SYNTHASE POLYPERTIDES

FILE REFERENCE: 07148-108001

CURRENT FILING DATE: 2010-06-08

PRIOR APPLICATION NUMBER: US 60/210,326

PRIOR APPLICATION NUMBER: US 60/210,326

PRIOR APPLICATION NUMBER: 2000-06-08

PRIOR PLING DATE: 2000-06-08

SEQ ID NO 30

LENGTH: 506
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US-09-877-476-36
US-09-877-476-36
Sequence 36, Application US/09877476
Patent No. 6713664
GENERAL INFORMATION:
APPLICANT: Blacklock, Brenda J.
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,326
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 506 amino acids from A. thaliana FAEI (SEQ ID
OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
OTHER INFORMATION: At K92R; hypothetical
US-09-877-476-36
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Pred. No. 19;
1; Mismatches
TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,326
NUMBER OF SEQ ID NOS: 56
NUMBER: PRICES FALLS FOR FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALLS FALL
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Matches 10; Conservative
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Sequence 156584,
Sequence 119916,
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
                                                                                                                                          November 10, 2004, 16:36:12; Search time 27.9309 Seconds (without alignments) 328.807 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/VS07 PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/NS06 NEW PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/NS06 NEW PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/NS07 NEW PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/NS07 NEW PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/NS08_NEW PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/NS08_NEW PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/NS08_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

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19: \cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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17 US-10-425-115-264584

15 US-10-425-115-264584

16 US-10-437-963-119916

19 US-09-877-476-10

16 US-10-758-524-10

16 US-10-758-524-10

16 US-10-758-524-10

17 US-09-877-476-12

18 US-09-877-476-12

19 US-09-877-476-12

19 US-09-877-476-12

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10 US-09-877-476-14
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123
1 GVSEAEGTFPLGTFLLGIASRLRSVA 26
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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17	47	8	0	σ	-09-877-476-2	equence 26,
18	47	ω,	0	თ	-09-877-476-3	equence 30,
19	47	œ,	0	σ	-09-877-476-3	equence 36,
20	47	œ	0	o	-09-877-476-3	equence 38,
21	47	œ.	0	σ	-09-877-476-4	equence 40,
22	47	œ,	0	15	S-10-276-977-	,
23	47	8	О	16	-10-758-524-	2,
24	47	ω.	0	16	-10-758-524-	æ
25	47	8	0	16	-10-758-524-1	12,
56	47	ω.	0	16	-10-758-524-	14,
27	47	ω.	0	16	-10-758-524-1	16,
28	47	8	0	16	-10-758-524-2	20,
29	47	æ	0	16	-10-758-524-2	22,
30	47	ω.	0	16	-10-758-524-2	24,
31	47	ω,	0	16	-10-758-524-2	26,
32	47	ω.	0	16	-10-758-524-3	30,
33	47	ω.	0	16	-10-758-524-3	36,
34	47	œ.	0	16	-10-758-524-3	38,
35	47	ω.	0	16	-10-758-524-4	40,
36	47	ω.	Н	16	-10-437-963-1515	151
37	47	ω.	4	76	-10-437-963-15152	151
38	ė.	7.	'n	15	-10-425-114-6	929
39	46.5	7.	S	15	-10-424-599-14604	146
40	46	7.	Н	17	-10-425-115-3558	355
41	46	7.	^	15	-10-282-122A-7658	765
42	46	۲.	α	σ	09-741-669-29	299,
43	46	7.	0	14	8-10-156-761-947	9470,
44	45	ė	σ	17	8-10-425-115-21797	equence 217978
45	45	ġ.	152	17	8-10-425-115-240	equence 24041
					ALIGNMENTS	
RESULT 1	RESULT 1	c				

Length 26; Sequence 4.2. Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
ITILE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US/00/092,750
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR PELING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 26 Indels 100.0%; Score 123; DB 14; 100.0%; Pred. No. 2.4e-12; iive 0; Mismatches 0; 1 GVSEAEGTFPLSTFLLGIASRLRSVA 26 Query Match Best Local Similarity 100.0 Matches 26; Conservative TYPE: PRT ORGANISM: Homo sapiens

1 GVSEAEGTFPLSTFLLGIASRLRSVA 26 RESULT 2
US-10-425-115-264584
; Sequence 264584 Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURENT APPLICATION NUMBER: US/10/437,963
CURENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 119916
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Pred. No. 1.4e+02;
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US-09-877-476-10

1 US-09-877-476-10

Sequence 10, Application US/09877476

Patent No. US20020049994A1

Patent No. US20020049994A1

APPLICANT: Javorski, Jan G.

APPLICANT: Blacklock, Brenda J.

TITLE OF INVENTION: RAITY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: RAITY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: RAITY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: STATHASE POLYPEPTIDES

FILE REFERENCE: 07148-108001

CURRENT FILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-06-08

PRIOR PILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: RESENSE for Windows Version 4.0
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Sequence 18, Application US/09877476
Sequence 18, Application US/09877476
Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18, Sequence 18
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US-10-437-963-119916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
39.0%; Score 48; DB 1
Best Local Similarity 45.0%; Pred. No. 1.46*
Matches 9; Conservative 5; Mismatches
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
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US-09-877-476-18
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LENGTH: 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 155062, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: A Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: VIALUATION NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-4-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 264
   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Thous
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 30-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 264584
LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.5%; Score 51; DB 17; Length 87; Best Local Similarity 44.8%; Pred. No. 3; Matches 13; Conservative 2; Mismatches 4; Indels
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US-10-424-599-155062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: MRT4577_172912C.1.pep
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wai
APPLICANT: Wu, Wai
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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TYPE: PRT ORGANISM: Artificial Sequence OTHER INFORMATION: 5' 74 amino acids from A. thaliana FAEI (SEQ ID OTHER INFORMATION: No.2) and 3' 431 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID No.4) having a mutation at COTHER INFORMATION: residue 306; designated At74 G306D; hypothetical US-10-758-524-18
           NUMBER OF SEQ ID NOS: 56
SOFFWARE: FaatSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 505
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                                                                                                                                                                                                                                                                                                                                                Query Match 38.2%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-877-476-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 5' 74 amino acids from A. thaliana FAE1 (SEQ ID OTHER INFORMATION: NO:2) and 3' 431 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At74
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Pred. No. 1e+02;
1; Mismatches 3; Indels
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Publication No. US20040139498A1

GENERAL INFORMATION:

APPLICANT: Jawarski, Jan G.

APPLICANT: Jawarski, Jan G.

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: PATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: PATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: PATTY ACID ELONGASE 3-KETOACYL COA

CURRENT APPLICATION: ONTHER : US/10/758,524

CURRENT APPLICATION NUMBER: US/877,476

PRIOR FILING DATE: 2004-01-15

PRIOR FILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
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Sequence 18, Application US/10758524

Publication No. US20040139498A1

GENERAL INFORMATION:

APPLICANT: Jaworski, Jan G.

APPLICANT: Jaworski, Jan G.

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: SYNTHASE POLYPERTIDES

FILE REPRENCE: 07148-108002

CURRENT APPLICATION NUMBER: US/10/758,524

CURRENT FILING DATE: 2004-01-15

PRIOR APPLICATION NUMBER: 09/877,476

PRIOR APPLICATION NUMBER: 60/210,326

PRIOR PELING DATE: 2000-06-08
SEQ ID NO 18
LENGTH: 505
TYPE: PRT
ORGANISW: Artificial Sequence
FEATURE:
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Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity 71.4%;
Matches 10; Conservative
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     Length 505;
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                                                          3; Indels
                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09877476

Sequence 2, Application US/09877476

Patent No. US20020049994A1

GENERAL INFORMATION:

APPLICANT: Jawarski, Jan G.

TITLE OF INVENTION: STATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: STATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: STATTY ACID ELONGASE 3-KETOACYL COA

FILE REFERENCE: 07148-108001

CURRENT TILING DATE: 20148-10801

PRIOR APPLICATION NUMBER: US 60/210,326

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

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MINDOR OF SEQ ID NO 2

MINDOR OF SEQ ID NO 2
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Patent No. US20020049994A1
General INFORMATION:
APPLICANT: Jaworski, Jan G.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA:
TITLE OF INVENTION: SYNTHAGE POLYPEPTIDES;
FILE REPERENCE: 07146-108001;
CURRENT APPLICATION NUMBER: US/09/877,476;
CURRENT APPLICATION NUMBER: US 60/210,326;
PRIOR APPLICATION NUMBER: US 60/210,326;
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56;
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 8;
LENGTH: 506
Score 47; DB 16;
Pred. No. 1e+02;
1; Mismatches 3;
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ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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US-09-877-476-16
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US-09-877-476-20
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                       NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa = Ala or Thr
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID
OTHER INFORMATION: 00:2) and 3' 392 amino acids from B. napus
OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAE1 (SEQ ID OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having mutations at OTHER INFORMATION: residues 91 and 92; designated At114 L91C K92R
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US-09-877-476-14
; Sequence 14, Application US/09877476
; Patent No. US-0020049994A1
; GENERAL INFORMATION:
APPLICANT: Jaworsk, Jan G.
; APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: SYNTHASE POLYBETIDES
; FILE REPERENCE: 07146-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
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APPLICANT: Blacklock, Brenda J.
TILE OF INVENTION: SYNTHASE DOLYPEPTIDES
TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
TITLE REFERENCE: 07148-108001
CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT FILING DATE: 2001-06-08
FRICK PILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 56
SOFTWARES: FASTSEQ for Windows Version 4.0
LENGTH: 506
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Pred. No. 1e+02;
1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
TENGTH: 506
TYPE: PRT
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1 Similarity 71.4%;
10; Conservative 1
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ORGANISM: Artificial Sequence
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Matches 10; Conserva
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Best Local Similarity
Matches 10; Conserv
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US-09-877-476-8
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PEATURE:
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having mutation at OTHER INFORMATION: residue 307; designated At114 G307D; hypothetical
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAE1 (SEQ ID OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus OTHER INFORMATION: elongase KCS (SEQ ID NO:4), having a mutation at OTHER INFORMATION: position 92; designated At114 K92R
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Patent No. US20020049994A1
Patent No. US20020049994A1
GENERAL INFORMATION:
APPLICANT: Blacklock, Brenda J.
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COATILE OF INVENTION: SINTHASE POLYPEPTIDES
FILE REPERENCE: 07148-108001
CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT PILING DATE: 2001-06-08
FRIOR PRILING DATE: 2000-06-08
FRIOR PRILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09877476

Sequence 16, Application US/09877476

Patent No. US20020049994A1

GENERAL INFORMATION

APPLICANT: Jaworski, Jan G.

APPLICANT: Blacklock, Brenda J.

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

TITLE OF INVENTION: FATTY SOUTHERPORTIDES

FILE REFERENCE: 07148-108001

CURRENY FILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-06-08

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOUTHARD: FASTSEQ for Windows Version 4.0
                                                                                                                                                                      Score 47; DB 9;
Pred. No. 1e+02;
1; Mismatches
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Pred. No. 1e+02;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 506
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Best Local Similarity 71.4%;
Matches 10; Conservative 1
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Best Local Similarity 71.4%;
Matches 10; Conservative 1
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23 FPLTAFLAGKASRL 36
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID
OTHER INFORMATION: NO:2) and 3' 392 amino acids from B. napus
OTHER INFORMATION: elongase KCS (SEQ ID NO:4) having mutations at
OTHER INFORMATION: positions 92 and 307; designated Ati14 K92R G307D;
US-09-877-476-22
FEATURE:
OTHER INFORMATION: 5' 114 amino acids from A. thaliana FAEI (SEQ ID)
OTHER INFORMATION: No.2) and 3' 392 amino acids from B. napus
OTHER INFORMATION: elongase KCS (SEQ ID NO.4) having mutations at
OTHER INFORMATION: positions 91, 92 and 307; designated At114 L91C
US-09-877-476-20
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Pred. No. 1e+02;
1; Mismatches 3; Indels
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38.2%; Score 47; DB 9; Length 506;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/09877476
Fatent No. US2020049994A1
GENERAL INFORMATION:
APPLICANT: Jaworski, Jan G.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COAFILE REFERENCE: 07148-108001
CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT APPLICATION NUMBER: US/09/877,476
CURRENT APPLICATION NUMBER: US 60/210,326
FRIOR APPLICATION NUMBER: US 60/210,326
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LANGTH: 506
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Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-877-476-22
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23 FPLTAFLAGKASRL 36 d

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Gaps

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Search completed: November 11, 2004, 01:28:23 Job time : 27.9809 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:29:32 ; Search time 5.79275 Seconds

(without alignments)

431.857 Million cell updates/sec
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431.857 Million cell upo 431.857 Million cell upo Perfect score: 123 Sequence: 1 GVSEAEGTFPLGIASRLRSVA 26

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283416 segs, 96216763 residues Total number of hits satisfying chosen parameters: 2834

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	conserved hypothet	hypothetical prote	S	probable membrane	stage V sporulatio	fatty acid elongas	translation elonga	probable translati	hypothetical prote	hypothetical prote	large atp-dependan	probable ATP-depen	programmed cell de	probable membrane	flagellar motor pr	conserved hypothet	flagellar biosynth			probable transport	aldehyde-ferredoxi	probable ABC trans	myb-like DNA-bindi	probable outer mem	apoptotic cell dea	membra	endonuclease III C	enodnuclease III [	hypothetical prote
SUMMAKIES	ID	B90497	H72769	T48162	A56641	G83827	T05272	T43434	T41343	AB1415	T45661	AC2637	B97419	859116	AE0326	G70386	H90052	G71290	G85943	B65072	C91098	C71078	H96622	T38479	33	B54437	AC3331	720	C86595	2645
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	Length	209	154	1467	275	487	506	513	1047	153	478	839	848	113	126	254	358	376	485	485	485	581	1469	556	853	113	123	209	209	466
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39.0%; Score 48; DB 2; Length 154;

Query Match

hypothetical prote	protein B0212.3 [i	replication licens	hypothetical prote	probable PPE prote	probable membrane	transcription regu	Na/taurocholate co	transporter (Pho87	hypothetical prote	conserved hypothet	hypothetical prote	probable ABC trans	hypothetical prote	RNA polymerase sig	apoptotic cell dea
T33743	G88651	C64345	A96750	B70520	S51464	G72298	155601	F70302	T29366	C82399	A11790	T35398	T22068	E82691	A54437
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36	36	36	36	36	35	3	35	35	35	8	35	35	35	35	35
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45															

# ALIGNMENTS

	RESULT 1 R90497
	conserved hypothetical protein [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus naviein 24 Max. 2001 #1500 Abanco Abanc
	C.Accession: B94497 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-'
-	Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to Genhank. April 2001
	A;Description: Sulfolobys solfataricus complete genome. A;Reference number: A99139 A;Accession: B9497
	A;Status: preliminary A;Molecule type: DNA A;Poseidner 1570
	A.Cross-references: UNIPROT:Q97U88; GB:AE006641; NID:g13816556; PIDN:AAK43233.1; GSPDB:G7 C;Genetics:
•	A;Gene: SSO3132 C;Superfamily: glyoxalase
	Query Match 41.1%; Score 50.5; DB 2; Length 209; Best Local Similarity 41.9%; Pred. No. 2.1; Matches 13; Conservative 5; Mismatches 8; Indels 5; Gaps 1;
	1 GVSBABGTFPLSTFLLGIASRLRSVA 26
	Db 62 GYNQIKRDFPSSTFLINEKDLGLLKRASSMA 92
	RESULT 2 H72769
	hypothetical protein APE0147 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Species: Aeropyrum pernix C;Date: 00, 20, 20, 20, 20, 20, 20, 20, 20, 20,
	C.bate: Zo-Aug-1299 #Bequence_revision Zo-Aug-1999 #text_cnange_09-004 C.Accession: H72769
	Kikawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaik awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki nwa pas. 6, 83101 1949
	A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A,Reference number: A72450; MUID:99310339; PMID:10382966
	A;Accession: H72769 A;Status: preliminary A;Molecule type: DNA
	A;Residues: Î-154 «KAW» A;Cross-references: UNIPROT:Q9YFV3; DDBJ:AP000058; NID:g5103388; PIDN:BAA79058.1; PID:d1 A;Experimental source: strain K1
	C;Genetics: A;Gene: Appol47 C:Gunerfamily: oneserved humotherical protein MIO281
	Cjsuperiamily: conserved hypothetical protein model

Best Local Matches 1

8

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RESULT 7
143434
14ranslation elongation factor EEF-3 - fission yeast (Schizosaccharomyces pombe) (fragment translation elongation factor EEF-3 - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
A.Reference number: A83650; MUID:20512582; PMID:11058132
A.Accession: G83627
A.Accession: Dealminary
A.Astatus: preliminary
A.Astatus: preliminary
A.Molecule type: DNA
A.Residues: 1-487 <STO>
A.Gross-references: UNIPROT:09KCZ6, GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB0514
A.Baction: BH1423
A.Gene: BH1423
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R,Uritani, M.; Shoumura, Y.; Yamada, S.
Biosci. Biotechnol. Biochem. 63, 769-772, 1999
A;Title: Detection and analysis of translation elongation factor 3 genes from various year A;Reference number: Z22510; MUID:99290044; PMID:10361693
A;Accession: T43434
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A;Experimental source: strain JY741
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T05272
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, Iews, HW, Mayer, K.P.X.; Schueller, C.
submitted to the Protein Sequence Database, Septembér 1998
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C,Superfamily: translation elongation factor 3; ATP-binding cassette
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Pred. No. 19;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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A;Residues: 1-506 <BEV>
A;Cross-references: UNIPROT.038860; EMBL:AL023094
A;Experimental source: cultivar Columbia; BAC clone T4L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: T4L20.100
C;Superfamily: very-long-chain 3-ketoacyl-CoA synthase
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Best Local Similarity 40.0%; Pred. No. 20;
Matches 10; Conservative 5; Mismatches 10
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A,Molecule type: DNA
A,Residues: 1-513 <URI>
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                                                                                                                                                                                                                                                                                                                                                      DB :
                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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Pred. No.
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50.0%;
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Best Local Similarity 50.09
Matches 11; Conservative
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Best Local Similarity
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A, Note: T4L20.100
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A;Note: nucleotide sequence not given; conceptual translation not complete
C;Superfamily: maltose transport protein malG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane transport protein - Clostridium perfringens
C;Species: Clostridium perfringens
C;Species: Clostridium perfringens
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession, A.L.; Blom, H.
R;Holck, A.L.; Blom, H.
B)NA Seq. 3, 191-194, 1992
A;Title: The nuclectide sequence of a putative membrane transport gene from Clostridium A;Reference number: A56641; MUID:93113001; PMID:1472712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Introns: 68/2; 121/3; 152/3; 178/1; 234/2; 291/3; 331/3; 516/3; 698/3; 721/3; 760/3;
2
                                                                                                                                                                                                                                                                                                                             hypothetical protein T1008.110 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 C;Accession: T48162 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, March 2000 A;Reference number: 224486 A;Reference number: T48162
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A;Status: preliminary
A;Moleune Cype: DNA
A;Residues: 1-1467 <BEV>
A;Cross-references: UNIPROT:Q9M033; EMBL:AL161746
A;Experimental source: cultivar Columbia: Par alm
                                                                     Pred. No. 3.9;
1; Mismatches
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Pred. No. 48;
2; Mismatches
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                                                                     ilarity 42.3%; Processive 4;
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Best Local Similarity 58.3%;
Matches 14; Conservative 2
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Best Local Similarity 38.53
Matches 10; Conservative
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A;Molecule type: DNA
A;Residues: 1-275 <HOL>
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A, Note: T1008.110

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large atp-dependant helicase-related protein [imported] - Agrobacterium tumefaciens (str. C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: Ac2637
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-839 «KUR»
A;Cross-references: UNIPROT:Q8UI06; GB:AE008688; PIDN:AAL41513.1; PID:g17738842; GSPDB:G:
A;Experimental source: strain C58 (Dupont)
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97419
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Lie, Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Cross_references: UNIPROT:Q8UI06; GB:AE007869; PIDN:AAK86307.1; PID:g15155423; GSPDB:GP
C;Genetics:
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       F.; Sal
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R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; WUID:21608550; PMID:11743193
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A;Experimental source: cultivar Columbia; BAC clone F13112
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Pred. No. 22;
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Pred. No. 39;
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50.0%;
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Best Local Similarity 52.2%;
Matches 12; Conservative
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Best Local Similarity 50.0%
Matches 15; Conservative
                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-478 <CHO>
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A; Introns: 255/3
A; Note: F13112.300
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C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Accession: AB1415
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
I.; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karet, U.
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Recession: AB1415
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-153 acua.
A;Cross-references: UNIPROT: Q873V8; GB:NC_003210; PIDN:CAD00936.1; PID:g16412223; GSPDB: A;EGnetics:
C;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                 probable translation elongation factor EF-3 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T41343
R;Vyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21970
A;Reference number: Z21970
A;Accession: T41343
A;Reference number: Z21970
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hypochetical protein F13112.300 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45661
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                                          GVSEAEGTFPLSTFLLGIASRLRSV
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Search completed: November 10, 2004, 13:40:49 Job time : 5.79275 secs
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                                                                                                                                                                                                                                                                                                                                                                                          Programmed cell death suppressor dad-1 - Caenorhabditis elegans

NAlternate names agene defender against cell death protein

Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S59116; T3742; S57513

R;Sudimoto, A.; Hozak, R.R.; Nakashima, T.; Nishimoto, T.; Rothman, J.H.

EMBO J. 14, 4434-4441, 1995; Nakashima, T.; Nishimoto, T.; Rothman, J.H.

A;Fitle: ada-1, an endogenous programmed cell death suppressor in Caenorhabditis elegans

A;Reference number: S59116; MUID:96003623; PMID:7556086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YPO2677 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession. AE0326
C;Accession. AE0326
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Wolecule type: mRNA
A;Residues: 1-13 sculo.
A;Cross-references: UNIPROT:P52872; EMBL:X89080; NID:g887395; PIDN:CAA61451.1; PID:g8873
R;Greco, T.; Elliott, G.; Keppler, D.
submitted to the RMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F57B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8ZDB1; GB:AL590842; PIDN:CAC92916.1; PID:g15980656; GSPDB:G
C;Genetics:
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A;Experimental source: strain Bristol N2; clone F57B10
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50.0%; Pred. No. 5.9;
tive 3; Mismatches
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A;Introns: 71/1
C;Superfamily: apoptotic cell death regulator DAD1
C;Keywords: apoptosis
                                                                                 ; Score 46.5; DB
; Pred. No. 39;
4; Mismatches
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C,Superfamily: hypothetical protein MJ1523
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A,Gene: AGR C 874
A,Map position: circular chromosome
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                                                                              Query Match 37.8%;
Best Local Similarity 52.2%;
Matches 12; Conservative 4
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Best Local Similarity
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A;Residues: 1-113 <GRE>
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A;Molecule type: DNA
A;Residues: 1-126 <KUR>
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-254 <AQF>
A;Coss.references: UNIPROT:067122; GB:AE000718; NID:g2983504; PIDN:AAC07083.1; PID:g2983:C;Genetics:
                                                                                                                                                                                                                                                                                                                               R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ové
                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70386
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70386
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Pred. No. 14;
1; Mismatches
                      Score 46; DB 2
Pred. No. 6.6;
3; Mismatches
                                                                                                                                                                                                                                                  flagellar motor protein MotA - Aquifex aeolicus
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                      37.48;
57.18;
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Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                         EGTFPLSTFLLGIA 19
                                                         Conservative
Query Match
Best Local Similarity
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Fri Nov 12 14:55:26 2004
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sequencing.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                         1825181 seqs, 575374646 residues
                                                                                                                                                                                                                    123
1 GVSEAEGTFPLSTFLLGIASRLRSVA 26
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Q8L703
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######################################	PRELIMINARY (TYEMBLYEL) (TYEMBLYEL) (TYEMBLYEL)  TOO 69803.  COO 69803.  COO 69803.  TOO 6701.	FROM N.A. G J.F., Eis (NOV-2003) 58648; AAR3 1PR0041812; 1PR007114; TIGR00710; PS50850; MF 402 AA; imilarity ; Conserva GVSEAEGTFPL   :::  GATASDGQLTL	PRELIMINARY 4 (TEMBLEEL. 4 (TEMBLEEL. 4 (TEMBLEEL. 1 Lance transpo. B03.87. 1 bacterium 58 environmental environmental ROM N.A;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. - EMBL; AY458643; AAR37935.1; -. SEQUENCE 429 AA; 44843 MW; E763DC581B810193 CRC64;
                                                                                                                  42.3%; Score 52; DB 2; illarity 52.6%; Pred. No. 17; Conservative 4; Mismatches
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Pred. No.
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KGSFPLSTIALGVAA 19
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OrderedLocusNames=SSO3132;
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Matches 9; Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                            Length 402;
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      SEQUENCE FROM N.A..
SEQUENCE FROM N.A..
Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.,
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY486648, AAR38338.1, -.
SEQUENCE 402 AA, 42022 MW, 9655B3DAD962D69F CRC64,
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SEQUENCE FROM N.A.

Heidelberg JF., Eisen J.A., Nelson W.C., DeLong B.F.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

BMBL, A458643, ARR379311, -..

InterPro; IPR004812; Efflux Bcr_CflA.

InterPro; IPR007114; MFS.

ITIGRENMS; TIGR00710; efflux Bcr_CflA; 1.

SEQUENCE #29 AA; 444843 MW; E763DC581B810193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DeLong E.F.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE FROM N.A.
Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Drug resistence transporter, Bcr/CflA family.
0RFNames=EBAC000-47H08.14;
uncultured bacterium 561.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Drug resistance transporter, Bor/CflA family.
EBAC000-47H08.14.
                                                                                                                                                                                                            Score 52; DB 2;
Pred. No. 16;
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Bacteria, environmental samples.
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Matches 10, Conservative
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STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=213296; PubMed=11427726;
She Q., Singh K.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
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No. [1]

No. [1]

Murakami K., Fuse H., Takimura O., Inoue H., Yamaoka Y.;

Murakami K., Fuse H., Takimura O., Inoue H., Yamaoka Y.;

Suburted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

1. SubcELIULAR LOCATION: Outer membrane (By similarity).

2. [1- SUBCELIULAR LOCATION: Outer membrane (By similarity).

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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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SEQUENCE FROM N.A.

Pubmed=15115801; DOI=10.1093/nar/gkh562;

Pubmed=15115801; DOI=10.1093/nar/gkh562;

Rolomay J.F., Rasko D.B., Mongodin E.F., Ravel J., DeBoy R.T.,

Rolomay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,

Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,

Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,

Porberger H.A., Tran B., Rathariou S., Wonderling L.D., Unlich G.A.,

Bayles D.O., Luchansky J.B., Fraser C.M.,

"Whole genome comparisons of serotype 4b and 1/2a strains of the food

borne pathogen Listeria monocytogenes reveal new insights into the

core genome components of this species.";

Nucleic Acids Res. 32:2386-2395(2004).
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBL_TaxID=265669,
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Pfam. PF00583; Acetyltransf 1; 1.
Complete proteome; Transferase.
SEQUENCE 153 AA; 17480 MW; A4D231EC38ED5CCF CRC64;
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NCBI_TaxID=265669;
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                                             SO DR READ BRILL BRIEF BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK B
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                               De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Koerara C.J., Median N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sansen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
PRIN: B90497.
InterPro; IPR001279; Blactmase-like.
Pfam; PP07973; Lactmanae-B.; I.
Complete protecome; Hypothetical protein.
SEQUENCE 209 AA; 23000 MW; AA863D463AB056A6 CRC64;
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MEDLINE=99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Kawarabayasi Y., Thio Y., Horikawa H., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nomura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
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Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales,
Desulfurococcaceae, Aeropyrum.
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SEQUENCE 154 AA; 17209 MW; 1D0C1270DA1D8BB7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Acetyltransferase, GNAT family.
OrderedLocusNames=LMOf2365 2710;
Listeria monocytogenes (serotype 4b / strain F2365).
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DNA Res. 6:83-101(1999).
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01-JUN-2003 (TrEMBLrel. 24, La
Hypothetical protein APE0147.
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Best Local Similarity 41.9%;
Matches 13; Conservative
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05-JUL-2004 (
05-JUL-2004 (
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01-NOV-1999
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Nelson K.E., Fouts D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J., White O., Nelson W.C., Nierman W., Beanan M.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selengut J., Van Aken S., Khouri H., Fedorova N.,
Porbegger H., Tran B., Kathariou S., Wonderling L.D., Unlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.,
"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species reveal new insights into the
Nucleic Acids Res. 32:2386-2395(2004).
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38.6%; Score 47.5; DB 2; Length 153;
Best Local Similarity 38.1%; Pred. No. 32;
Matches 16; Conservative 2; Mismatches 5; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria monocytogenes str. 4b F2365.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AA; 17480 MW; A4D231EC38ED5CCF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 DMEGTFHLGAFEKDVLLGIASFYPEKSTVIMNPAQYRIRGVA 75
4 EAEGIFPLSTF----LLGIAS------RLRSVA 26
                                                             34 DMEGTFHLGAFEKDVLLGIASFYPEKSTVIMNPAQYRIRGVA 75
                                                                                                                                                                                                                                                                                                                                                                  10-WAY-2004 (TrEMBLrel. 27, Created)
10-WAY-2004 (TrEMBLrel. 27, Last sequence update)
10-WAY-2004 (TrEMBLrel. 27, Last annotation update)
Acetyltransferase, GNAT family.
                                                                                                                                                                                                                                                                                            153 AA
                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Nakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
                                                                             Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MR-2002 (TrEMBLrel. 20, Created)
1-MR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
putaive copia-like retrotransposon polyprotein, 5'-partial
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                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus halodurans.
Bacteria; Firmitutes; Bacillales; Bacillaceae; Bacillus.
VCBI_TaxID=86665;
275 AA; 30699 MW; CC6B951258772772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Stage V sporulation protein AF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 AA
                                                                             Score 47; DB
Pred. No. 68;
3; Mismatches
                                                                                                                                                                                                                                                                                                                146 GIVSAFGTPLIRQFFMGLPKELEEAA 171
                                                                                                                                                                                                                                   1 GVSEAEGTFPLSTFLLGIASRLRSVA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AVGTFATPSYELGLANRLIRVA 415
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                                                                         Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
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Matches 11; Conservative
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SEQUENCE FROM N.A.
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Q9KCZ6
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T1008_110.
Name=T1008_110;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta, Widiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; rosids, eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
Lemcke K., Mayer K.F.X.; F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ORF for putative membrane transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp.
PROSITE; PS50928; ĀBC_TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 AA.
                                                                                     PRT; 1467 AA
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STRAIN-NCTC8239;
MEDLINE-93113001; PubMed=1472712;
                                                                                     PRELIMINARY;
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        RESULT 10
Q9M033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=WS;
MEDLINE=95252821; PubMed=7734965;
James D.W. Jim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
"Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
gene with the maize transposon activator.";
Plant Cell 7:309-319(1995).
                                                                                                                                                                                                                                                                                               Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-Jub-2004 (TrEMBLrel. 27, Last annotation update)
Fatty acid elongase 1.

Name-Fael; Synonyms-AT4g34520, T4L20.100;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.

Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R. De Keyer A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                           ch 38.2%; Score 47; DB 2; Length 491
1 Similarity 57.9%; Pred. No. 1.2e+02;
11; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U29142; AAA70154.1;
EMBL; AL023094; CAA18331.1;
EMBL; AL025094; CAB80169.1;
                                                                            the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         1
491 AA; 55838 MW; 3C18C544FCEFE397 CRC64;
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G0; G0:0004415; F:acyltransferase activity;
G0; G0:0016740; F:transferase activity; IEA.
G0; G0:0009058; P:biosynthesis; IEA.
Interpro; IPR001099; N-C synthass.
Pfem; PFC72797; Chal sti Synt C; 1.
SEQUENCE 506 A4; 56263 MW; 4516D0EF8E453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 AA.
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                                                                                                                                                                                                                                                                                                                                                                                      79 ENVFPLSKFHSNAGSRLRS 97
[2]
SEQUENCE FROM N.A.
Buell'R.;
Submitted (NOV-2001) to the El
EMBL; AC091749; AAL31076.1; -
Gramene; Q8W5D1; -.
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Best Local Similarity
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                                                                                                                                                  Polyprotein.
NON TER
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0238860
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A lafontaine I., de Montigue J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.,
T "denome evolution in yeasts.",
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2014 (TrEMBLrel. 28, Last annotation update)
01-0CT-2014 (TrEMBLrel. 28)
01-0CT-2014 (TrEMBLrel. 28)
01-0CT-2014 (TrEMBLrel. 28)
01-0CT-2014 (TrEMBLrel. 28)
01-0CT-2014 (TrEMBLrel. 28)
01-0CT-2014 (TrEMBLrel. 28)
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Pred. No. 1.3e+02;
3; Mismatches 5; Indels
      Length 506;
Score 47; DB 2; Length 506
Pred. No. 1.2e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382135; CAG86550.1; -.
SEQUENCE 532 AA; 59070 MW; 47DC9639E0F25FE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                          532 AA.
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115 GVSEIVATLPLTLFVIG 131
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Similarity 52.9%;
9; Conservative
   Query Match 38.2%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                              FPLTAFLAGKASRL 36
                                                                                                                                   9 FPLSTFLLGIASRL 22
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Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              sw model
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November 10, 2004, 12:32:37; Search time 10.7081 Seconds (without alignments)
191.991 Million cell updates/sec

US-10-092-750-43 156 1 RAPRFIKQILLDLKREIDFNVRLVEYFNPLS 31 Title:
Perfect score: 1
Sequence: 1

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

478139 segs, 66318000 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\*
1: /cgn2\_6/ptodated/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodated/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodated/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodated/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodated/1/iaa/PCTUS COMB.pep:\*
6: /cgn2\_6/ptodated/1/iaa/PCTUS COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	nce	Sequence 3268, Ap	Sequence 13195, A	Seguence 17253, A	equence	Sequence 4, Appli	equence	Sequence 4, Appli	equence	equence		equence 5, Appl	ednence	n)	ednence			equence	34,	equence 7,	7	equence 4,	equence 2,	4.	equence 2,	equence 4,	e 15,
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## ALIGNMENTS

1. Sequence 4, Application US/09580929 1. Sequence 4, Application US/09580929 1. Parent No. 658290 1. GENERAL INFORMATION: 1. APPLICANT: Lam, Joseph S. 1. APPLICANT: Lam, Joseph S. 1. TITLE OF INVENTION: Whype and Method for Assay of WbpP FILE REPERBANCE: 6580-189 1. CURRENT APPLICATION NUMBER: US/09/580,929 1. CURRENT FILING DATE: 1999-05-26 1. PRIOR PILING DATE: 1999-05-28 1. NUMBER: OF SEQ ID NOS: 7 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 4 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SEQ ID NO 9 1. SE							ם													
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US-09-580-923-4 Sequence 4, Application Sequence 4, Application GENERAL INFORMATION: APPLICANT: Lam JOSE APPLICANT: Creuzener TITHE OF INVENTION: FILE REPERENCE: 65 CURRENT APPLICATION: 1 CURRENT APPLICATION IN CURRENT FILING DATE: NUMBER OF SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS SEQ ID NOS		E C			qde			30-1	TOMB	20	<b>HBER</b>	199		ver						
US-09-580-929-4 Sequence 4, Application of Settler No. 6582910 Settler No. 6582910 Settler No. 6582910 Settler No. 6582910 SETTLE OF INVENTION OF FILE REPERSORE CURRENT APPLICATION OF PRIOR PELING DAPPLICATION PRIOR PILING DATE NOWBER OF SEQ ID SOFTWARE: Peten SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 4 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ ID NO. 6 SEQ		ati		 Z	Jose	ene	ä	9	g	Ξ:	Ē		NOS	tIn						
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Query Match
Best Local Similarity 46.2%; Pred. No. 0.33;
Matches 12; Conservative 8; Mismatches 5; Indels

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Gaps

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US-09-583-110-3268

Sequence 3268, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REPERENCE: PATHON-07A

CURRENT APPLICATION NUMBER: US/09/583,110

FRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

FRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3268

LENGTH: 339

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Gaps
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                                                                   Sequence 4, Application US/08861464
; Sequence 4, Application US/08861464
; Patent No. 5874210
; GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Rennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senescence
TITLE OF INVENTION: in Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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APPLICANT: Cole, Francesca
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senesence in
NUMBER OF SEQUENCES: 16
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 2-AAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/396,001
FILING DATE: 28-FEB-1995
PRIOR APPLICATION NUMBER: US/08/396,001
FILING DATE: 28-FEB-1995
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/08/107,408
FILING DATE: 15-AUG-1994
PRIOR APPLICATION NUMBER: US/08/107,408
FILING DATE: US-AUG-1993
ATTONNEY/AGENT INFORMATION:
ANAME: CENTRAL DESTRICTS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Austriaco Jr., Nicanor
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Patent No. 5919618
GENERAL INPORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nican
APPLICANT: Claus, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
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Cole, Francesca
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Best Local Similarity 55.65
Matches 15; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-861-464-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                          US-08-861-464-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-396-001-4
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APPLICANT: Kelth Weinstock et al

APPLICANT: Kelth Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TILE REPERENCE: 1071966.13

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PERLACATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13195
LENGTH: 363
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                                                                                                                                                                                       Length 339;
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Pred. No. 2.4;
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                                                                                                                                                                                       Score 58.5; DB 4;
Pred. No. 0.66;
9; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11195, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
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; Sequence 17253, Application US/09248796A
; Patent No. 6747137
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
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l Similarity 42.3%;
11; Conservative 9
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Best Local Similarity 38.7%;
Matches 12; Conservative
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US-09-248-796A-17253
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Best Local Similarity
Matches 11; Conserv
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US-09-489-039A-13195
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APPLICANT: Glaus, James J.
APPLICANT: Glaus, James J.
APPLICANT: Claus, James J.
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: CENEST DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: 1991-003
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1994-08-15
PRIOR FILING DATE: 1994-08-15
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
SCOTVARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.0%; Score 53; DB 2; Length 834; Best Local Similarity 55.6%; Pred. No. 13; Matches 15; Conservative 4; Mismatches 6; Indels
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                                                                                                                           COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,001
FILING DATE: US-FEB.1995
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TEMPERANCE CHARACTERISTICS:
TEMPERANCE CHARACTERISTICS:
     Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 YIIQFLLDIK-ELDFYL-LAELFNRLS 416
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ORGANISM: Saccharomyces cerevisiae
ADDRESSEE: Hamilton, Broo
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                     RY: USA
02173
                                                                            STATE: MA
COUNTRY:
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Gaps Gaps GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guarence, Leonard P.
APPLICANT: Claus, James J.
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANTON: YEAST
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050.1491-005
CURRENT APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1994-06-15
PRIOR FILING DATE: 1994-06-15
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-08-16
PRIOR PILING DATE: 1993-06-01
NUMBER OF SEC ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 834 ij Score 53; DB 4; Length 834; Pred. No. 13; 4; Mismatches 6; Indels 8; Indels RESULT 9
US-09-723-546-9
i Sequence 9, Application US/09723546
i Sequence 9, Application US/09723546
i Patent No. 6737239
i GENERAL INFORMATION:
i APPLICANT: Clark, Mike A
i TITLE OF INVENTON: Modified Arginine Deiminase
i FILE REFERENCE: PHOSO059
i CURRENT APPLICATION NUMBER: US/09/723,546
i CURRENT FILING DATE: 2000-11-28
i PRIOR APPLICATION NUMBER: 09/023,809
i PRIOR FILING DATE: 1998-02-13
i NUMBER OF SEQ ID NOS: 14
i SEQ ID NO 9
i LENGTH: 409 33.0%; Score 51.5; D 34.5%; Pred. No. 9.6; tive 10; Mismatches 4 RFIKOILLDLKREIDFNVRLV-EYFNPLS 31 392 YIIQFLLDIK-ELDFYL-LAELFNRLS 416 5 FIKQILLDLKREIDFNVRLVEYFNPLS 31 TYPE: PRT ; CRGANISM: Saccharomyces cerevisiae; US-09-826-752-4 Sequence 4, Application US/09826752 Patent No. 6787300 Query Match
Best Local Similarity 55.6%;
Matches 15; Conservative rype: prr; ORGANISM: Borrelia afzelii US-09-723-546-9 Query Match
Best Local Similarity 34.5
Matches 10; Conservative 셤

5 FIKQILLDLKREIDFNVRLVEYFNPLS 31

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Sequence 9, Application US/09124141

1 Sequence 9, Application US/09124141

1 Sequence 9, Application US/09124141

2 Sequence 9, Application US/09124141

3 Fatent No. 6211352

3 GENERAL INFORMATION:
APPLICANT: Harrison, Leonard
APPLICANT: Honeyman, Margot
APPLICANT: Carm, David denty
APPLICANT: De Aizpurua, Henry
TITLE OF INVENTION: ACID DECARBOXYLASE AUTOANTIGEN ASSOCIATED DISEASES
TITLE OF INVENTION: ACID DECARBOXYLASE AUTOANTIGEN ASSOCIATED DISEASES
TITLE OF INVENTION: ACID DECARBOXYLASE AUTOANTIGEN ASSOCIATED DISEASES
TITLE OF INVENTION: ACID DECARBOX DECIDATION NUMBER: US/09/124,141

CURRENT FILING DATE: 1998-07-29

EARLIER FILING DATE: 1994-09-20

EARLIER APPLICATION NUMBER: 07/839,805

EARLIER APPLICATION NUMBER: 07/839,805

EARLIER PILING DATE: 1992-02-21

NUMBER OF SEQ ID NOS: 34

COFTMARE: PATENTING DATE: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                     COMPUTER: PREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSIPLATION NUMBER: US/08/766,858A
FLING DATE: 13-DEC-1996
CLASSIPLATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,545
PILING DATE: 13-FEB-1996
ATTORNEY AGENT INPORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3301-4-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: LEGIONELLA PNEUMOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.4%; Score 47.5; D
Best Local Similarity 45.8%; Pred. No. 58;
Matches 11; Conservative 6; Mismatches
                    NUMBER OF SECURICES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STRATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QILLDLKREIDFNVRLVEYFNPLS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 575 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
LENGTH: 203
TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-766-858A-5
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
DUCCELE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-11-08
RIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                               Sequence 175. Application US/09710279

Sequence 175. Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:
APPLICANT KINMERIN, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT APLICATION NUMBER: 60,164,258

PRICR APPLICATION NUMBER: 60,164,258

PRICR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1756

LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence: synthetic // OTHER INFORMATION: amino acid sequence US-09-710-279-1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.1%; Score 50; DB 4; Length 338; 31.2%; Pred. No. 13; tive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 50; DB 3; Length 406; 31.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /GS-08-766-858A-5
// Sequence 5, Application US/08766858A
// Sequence 5, Application US/08766858A
// Patent No. 5935782
// GENERAL INFORMATION:
// APPLICANT: Cianciotto, Nicholas P.
// APPLICANT: Hickey, Erin K.
// APPLICANT: O'Connell, William A.
// TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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; Sequence 3202, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Staphylococcus epidermidis US-09-134-001C-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.4.
Best Local Similarity
Conservative
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Best Local Similarity 31.2
Matches 10; Conservative
                                  RESULT 10
US-09-710-279-1756
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT PELLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harrison, Leonard
APPLICANT: Harrison, Leonard
APPLICANT: Cram, David
APPLICANT: Cram, David
APPLICANT: Cram, David
APPLICANT: Cram, David
APPLICANT: De Alzpurua, Henry
TITLE OF INVENTION: A METHOD FOR THE DIAGNOSIS AND TREATMENT OF GLUTAMIC
TITLE OF INVENTION: ACID DECARBOXILASE AUTOANTIGEN ASSOCIATED DISEASES
TITLE OF INVENTION: ACID DECARBOXILASE AUTOANTIGEN ASSOCIATED DISEASES
FILE REFERENCE: Phillips, Ormonde & Fitzpatrick
CURRENT APPLICATION NUMBER: U8/09/124,141
CURRENT APPLICATION NUMBER: 08/308,952
EARLIER FILING DATE: 1994-09-20
EARLIER FILING DATE: 1994-09-20
EARLIER FILING DATE: 1992-02-21
NUMBER OF SEQ ID NOS: 34
SOCTHARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 250
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                                                           Gaps
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(7)
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Query Match 30.1%; Score 47; DB 3; Length 203; Best Local Similarity 35.5%; Pred. No. 20; Matches 11; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
30.1%; Score 47; DB 3; Length 250;
Best Local Similarity 35.5%; Pred. No. 26;
Matches 11; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.1%; Score 47; DB 3; Length 226; Best Local Similarity 41.7%; Pred. No. 23; Matches 15; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FIKOILL-----DLKREI---DFNVRLVEYFN 28
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                                                                                                                                              161 PESLEQILVDCRDTLKYGVRTGHPRFFNOLS 191
                                                                                                             3 PRFIKQILLDLKREIDFNVRL--VEYFNPLS 31
                                                                                                                                                                                                                                                                                                   Sequence 5494, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09124141
Patent No. 6211352
GENERAL INFORMATION:
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                   RESULT 14
US-09-134-001C-5494
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Search completed: November 10, 2004, 13:44:12 Job time : 11.7081 secs

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Sequence 588, App Sequence 2, Appli Sequence 178842,

Sequence 5045, Appsequence 179426, Appsequence 47644, Appliated 23005, Sequence 23005, Sequence 10, Appliated 23008, Sequence 10, Appliated 200, Appsequence 10, Appliated 200, Appsequence 105103, Sequence 5752, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753, Appsequence 5753,

46425, A 47711, A 104894, 1326, Ap

Sequence 4 Sequence 4 Sequence 1 Sequence Sequence

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Sequence:

Searched:

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US-10-092-750-43

Sequence 43, Application US/10092750

Publication No. US20030032157A1

Sequence 41, Application W. US2030032157A1

APPLICANT: Hammond, Philip W. APPLICANT: Alpin, Unlia

TILE REFERENCE: 50036/05000

FILE REPERENCE: 50036/05000

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT PILING DATE: 2002-03-07

PRIOR PILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 31
6 US-10-451-467A-588

4 US-10-060-275-2

5 US-10-282-122A-50612

4 US-10-369-423-5349

4 US-10-369-42-6179426

5 US-10-424-599-179426

5 US-10-424-599-179426

5 US-10-424-599-2005

5 US-10-425-114-47644

5 US-10-425-114-47644

6 US-10-674-666-16

6 US-10-674-666-16

6 US-10-674-666-16

7 US-10-739-9232008

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6 US-10-674-666-16

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9 US-10-425-114-46883

9 US-10-282-122A-47711

9 US-10-369-493-1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
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US-09-864-761-34496
US-09-864-761-34496
; Sequence 34496, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
      ORGANISM: Homo sapiens
   US-10-092-750-43
    Sequence 43, Appl
Sequence 24, App
Sequence 22, App
Sequence 22, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 1462, Ap
Sequence 1462, Ap
Sequence 214640,
Sequence 24460,
Sequence 34660, Appli
Sequence 34660, Appli
Sequence 3663, Appli
Sequence 3666, Appli
                                                                                                                           (without alignments)
328.807 Million cell updates/sec
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                                                                                                           November 10, 2004, 16:36:12 ; Search time 33.3022 Seconds
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-114-44206
US-10-739-930-8963
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US-10-09-864-761-34496

US-10-022-8284-257

4 US-10-025-201-3

4 US-10-012-6008-221

6 US-10-114-270-30

US-09-867-550-1462

US-09-318-271-8
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156
1 RAPRFIKQILLDLKREIDFNVRLVEYFNPLS 31
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                               using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Indels

11111 1224500000128

Result 80.

Length 31;

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APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Salceda, Susana
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Prc.
FILE REFERENCE: DEX-024
CURRENT FILING DATE: 2002-07-09
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 266
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10025201
Publication No. US20030003468A1
GENERAL INFORMATION:
APPLICANT: Crow, Mary K.
TITLE OF INVENTION: MARKERS FOR DISEASE SUSCEPTIBILITY AND TARGETS FOR THERAPY
CURRENT APPLICATION NUMBER: US/10/025,201
CURRENT FILING DATE: 2001-12-19
PRIOR PLILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank Accession No. US20030003468A1 U09116
DATABASE ENTRY DATE: 1995-02-02
RELEVANT RESIDUES: (1)..(1275)
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llarity 54.8%; Pred. No. 0.018;
Conservative 7; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.3%; Score 78.5; DB 14; Length 1031; 54.8%; Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 APRFIKQILLDLKREIDFNVRLVEYFN-PLS 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 APRFIKQILLDLKREIDFNVRLVEYFN-PLS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
             24 APKFIKQLLIDLRNEIDSNIVIVGNFN 50
                                                                                                                                                                                                                     Sequence 257, Application US/10082828A Publication No. US20030175715A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-828A-257
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                US-10-082-828A-257
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                           APPLICANT: PERIN, SDAITON G.
APPLICANT: PERIN, SDAITON G.
APPLICANT: HEAR, DAVIG G.
APPLICANT: HEAR, DAVIG G.
APPLICANT: HEAR, DAVIG G.
APPLICANT: HEAR, DAVIG GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID G. 23
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-05-27
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PRIOR PELING DATE: 2001-01-30
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PRIOR PE
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HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
HER INFORMATION: EXPRESSED IN PRAIN, SIGNAL = 2
HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN HT474, SIGNAL = 6.9
HER INFORMATION: EXPRESSED IN HELLOON SIGNAL = 5.6
HER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.7
HER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.1
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN HILA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.5
HER INFORMATION: SYST HUMAN HIT: AMS6328.1, EVALUE 4.00e-59
HER INFORMATION: SWISSPROT HIT: PO8548, EVALUE 1.00e-51
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Best Local Similarity 59.3%; Pred. No. 0.00016;
Matches 16; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SUFFARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34496
LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO AC006459.2
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ORGANISM: Homo sapiens
FEATURE:
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; Sequence 221, Application US/10012600B; Publication No. US20030064377A1

RESULT 5 US-10-012-600B-221

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Gaps

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APPLICANT: JJ, Weishen
APPLICANT: Anderson, David W.
APPLICANT: Rateles, Mario W.
APPLICANT: Rateles, Mario W.
APPLICANT: Ratelli, Luca
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Scone, David J.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: NOUNBER: US/10/114,270
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICANTON NUMBER: 60/281,366
PRIOR PELING DATE: 2001-04-05
PRIOR PELING DATE: 2001-04-06
PRIOR PELING DATE: 2001-04-06
PRIOR APPLICANTON NUMBER: 60/282,930
PRIOR APPLICANTON NUMBER: 60/282,930
PRIOR APPLICANTON NUMBER: 60/282,930
PRIOR APPLICANTON NUMBER: 60/282,930
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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46.5%; Score 72.5; D

Best Local Similarity 51.6%; Pred. No. 0.13

Matches 16; Conservative 7; Mismatches
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Application US/10114270
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Casman, Stacie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Padigaru, Muralidhara
Shimkets, Richard A.
Gangolli, Esha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                             Vernet, Corine
Zerhusen, Bryan D.
Gorman, Linda
Shenoy, Suresh G.
                                                                                                      APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Killer, Charles E.
APPLICANT: Malyankar, Uniel M
APPLICANT: Spytek, Kimberly A.
                                                                                                                                                                                                                                                                                               Patturajan, Meera
Liu, Ziaohong
Gusev, Vladimir Y.
Li, Li
                                           US20040030110A1
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US-10-114-270-30
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                                   APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REPRENCE: DEX-0265
CURRENT APPLICATION NUMBER: US/10/012,600B
PRIOR FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin version 3.1
SEQ ID NO 221
LENGTH: 363
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47.1%; Score 73.5; DB 16; Length 1274;
Best Local Similarity 53.3%; Pred. No. 0.095;
Matches 16; Conservative 7; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.4%; Score 74; DB 14; Length 363; Best Local Similarity 51.7%; Pred. No. 0.021; Matches 15; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION

APPLICANT: INCYTE CORPORATION

APPLICANT: BUGGHN, Mariah R.

APPLICANT: SUE, Henry

APPLICANT: TWE, Henry

APPLICANT: U, Yan

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TAL, Preeti G.

TITLE OF INVENTION: NUCLEIC ACID MODIFICATION ENZYMES

FILE REFERENCE: P1-0280 USN

CURRENT FAPLICATION NUMBER: US/19/415,615

CURRENT FILING DATE: 2003-04-29

PRIOR FILING DATE: 2001-11-01

PRIOR FILING DATE: 2000-11-02

PRIOR FILING DATE: 2000-11-02

PRIOR FILING DATE: 2000-11-02

PRIOR FILING DATE: 2000-11-02

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PRIOR FILING DATE: 2000-11-02
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; OTHER INFORMATION: Incyte ID No: 1258887CD1
US-10-415-615-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 APRFIKQILLDLKREIDFNVRLVEYFNPL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10415615 Publication No. US20040101943A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-012-600B-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
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117 APTFIKQVLSDLQRDLDSHTLIMGDFNTFLS 147

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RESULT 7 US-10-114-270-30

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURENT APPLICATION NUMBER: US/10/424,599
CURENT APPLICATION DATE: 2003-04-28
SEQ ID NOS: 285684
APPLICANT: Berry, Alan APPLICANT: Berry A. Alan APPLICANT: Berry, Alan APPLICANT: Berry, Alan APPLICANT: Burning, Jeffrey A. APPLICANT: Severson, David K. APPLICANT: Burlingame, Richard P. TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS" TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS" FILE REPRENCE: 3161-24
CURRENT APPLICATION NUMBER: 60/125,073
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 60/088,549
EARLIER PILING DATE: 1998-06-08
SEALLER FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35847C.1.pep
US-10-424-599-214640
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156 VEQILTDLQKAQPDWSIALLRYFNPV 181
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kou, Yinua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.23
Matches 12, Conservative
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ORGANISM: Glycine max
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US-10-424-599-214640
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Fatent No. US20020082266AI

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT Leach, Martin D.
APPLICANT Leach, Pamela
APPLICANT Law, Debbie
APPLICANT Topper, James
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICANT 2000-03-03
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FateSEQ for Windows Version 4.0
SEQ ID NO 1462

LEACH: 78
THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY THEREBY T
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OTHER INFORMATION: Wherein Xaa may be any one of Ala or Arg or Asn or Asp or Cys or
OTHER INFORMATION: His or Ile or Leu or Phe or Pro or Ser or Thr or Tyr or Val
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42.0%; Score 65.5; DB 14; Length 148;
Best Local Similarity 51.6%; Pred. No. 0.14;
Matches 16; Conservative 5; Mismatches 9; Indels 1
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                                                                    Sequence 2911, Application US/10104047
Publication No. US20030236392A1
CENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 APRLIKQVLRDRQRDLDSHTITVGDFNMPLS 133
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19 RAPRYIKQI-LDLRRVIDSKTIKAADFN 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-104-047-2971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-867-550-1462
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US-09-318-271-8; Sequence 8, Application US/09318271A; Patent No. US20020012979A1

RESULT 10

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PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: Patentin version 3.1
SEQ ID NO 588
                                                                                                                                                                                            US-10-451-467A-588
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APPLICANT: CONTERRAS, ROLAND HENRI
APPLICANT: CONTERRAS, ROLAND HENRI
APPLICANT: CONTERRAS, ROLAND HENRI
APPLICANT: LUYTEN, WALTER HERWAN WARIA LOUIS
APPLICANT: LUYTEN, WALTER HERWAN WARIA LOUIS
APPLICANT: REEKGANS, RIEKA JOSEPHINA
TITLE OF INVENTION: SAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-4
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870002.1
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Sequence 8963; Application US/20040216190A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: 38-21 [53377] B

CURRENT APPLICATION NUMBER: 105/10/739,930

CURRENT FILING DATE: 2003-12-18

SEQ ID NO 8963

LENGTH: 351
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(531313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 44206
LENGTH: 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: GLYMA-23APR03-C2735_7.P
US-10-739-930-8963
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.9%; Score 57.5; DB 15; Best Local Similarity 35.5%; Pred. No. 3.1; Matches 11; Conservative 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 700889134_FLI.pep
US-10-425-114-44206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RAPRFIKOILLDLKR-EIDFNVRLVEYFNPL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RAPRFIKQILLDLKR-EIDFNVRLVEYFNPL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 588, Application US/10451467A Publication No. US20040161840A1
                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-739-930-8963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-451-467A-588
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                                                                     Score 55; DB 16; Length 337;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                             9; Indels
                                                                                                                                                                                                                                        US-10-060-275-2

US-10-060-275-2

Sequence 2, Application US/10060275

Publication No. US20030073828A1

GENERAL INPORMATION:
APPLICANT: BAI, LIFANG

APPLICANT: HOCKER, BEINERANS.
TITLE OF INVENTION: BEPREARSE GENE AND USE THEREOF
FILE REFERENCE: 059440-0143

CURRENT FILING DATE: 2002-06-11

PRIOR APPLICATION NUMBER: 60/265,311

PRIOR FILING DATE: 2001-02-01

PRIOR FILING DATE: 2001-02-01

NUMBER OF SEQ. ID NOS: 8

SOFTWARE: PATENTING DATE: 201-02-01

SEQ ID NO 2: 8

SEQ ID NO 2: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.5; DB 14;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RAPRFIKQILLDL-KREIDFNVRLVEYFNPL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 11, 2004, 01:28:24 Job time : 34.3522 secs
                                                                                                                                                                       1 RAPRFIKQILLDLKREIDFNVRLV 24
                                                                     Query Match
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.5%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Solanum tuberosum
TYPE: PRT
ORGANISM: Candida albicans
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 6.90674 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-43 156 1 RAPRPIKQILLDLKREIDFNVRLVEYFNPLS 31 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ы	line-1 protein ORF	reverse transcript	reverse transcript	retrovirus-related	Э,	UDPglucose 4-epime	UDP-galactose-4-ep	UDP-galactose-4-ep	UDP-glucose 4-epim	UDPglucose 4-epime	UDPglucose 4-epime	hypothetical narbo	nodulin - fava bea	ď		٧.	9	ical	isof	probable reverse t	hypothetical prote		UDPglucose 4-epime		ü	4-e	UDPglucose 4-epime	4
SUMMARIES		B28096	I38588	S65824	GNHUL1	B34087	XUECUG	C90727	D85578	B95187	C98054	T10496	S49879	T12157	849898	A37760	851328	AF0594	T19989	T12156	S16788	378	177	7074	T32023	6419	0652	B86261	6278
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TS18.7 protein - A	4-epi	UDPglucose 4-epime	transcription-repa	UDPglucose 4-epime	hypothetical prote	hypothetical narbo	UDP-glucose 4-epim	formate hydrogenly	unknown protein T1	conserved hypothet	UDPglucose 4-epime	conserved hypothet	hypothetical prote	UDPglucose 4-epime	probable 3-isoprop
E86431	A64063	T08911	D84964	AB0140	F81302	S49880	F82419	F69151	A96722	H70380	T10588	E71284	A71215	D69628	E71180
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419	338	350	812	338	466	285	338	370	676	253	379	456	507	339	323
33.3	33.0	33.0	33.0	32.4	32.4	32.1	31.7	31.7	31.7	31.4	31.4	31.4	31.4	31.1	30.8
52	51.5	51.5	51.5	50.5	50.5	20	49.5	49.5	49.5	49	49	49	49	48.5	48
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Line-1 protein ORF2 - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: O3-Nov-1988 #text_change 09-Jul-2004 C.Species: O3-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004 C.Sacession: B28096 R.Skowronski, J.; Fanning, T.G.; Singer, M.F. Mo.F. Cell. Biol. 8, 1385-1397, 1388 A.Steference number: A28096; MUID:88246405; PMID:2454389 A.Stecession: B28096 A.Stecession: B28096 A.Stetus: preliminary, not compared with conceptual translation A.Stetus: preliminary not compared with conceptual translation A.Stetus: 1-1275 A.SKO.A.A.Stotus: 1-1275 A.SKO.A.A.Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:O00363; UNIPROT:Q9YSKO; UNIPROT:Q00366; UNIPROT:Q8TE30; UNIPROT:Q00375
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Query Match 50.3%; Score 78.5; DB 2; Length 1275; Best Local Similarity 54.8%; Pred. No. 0.012; Matches 17; Conservative 7; Mismatches 6; Indels 1;

1; Gaps 2 APRFIKOILLDLKREIDFNVRLVEYFN-PLS 31 ઠે

121 APRFIKQVLSDLQRDLDSHTLIMGDFNTFLS 151

RESULT 2

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NyAlternate names: ORF2 protein
NyAlternate names: ORF2 protein
Cippecies: Homo sapiens (man)
Cippecies: Homo sapiens (man)
Cipate: O2-Unl-1996 #text\_change O9-Unl-2004
Cipate: O2-Unl-1996 #sequence\_revision O2-Unl-1996 #text\_change O9-Unl-2004
Cipate: O2-Unl-1996 #sequence\_revision C.Un.; Boehm, C.D.; Kazazian, H.H.
Rifolmes, S. E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
A;Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q p;
A;Reference number: 138586
A;Acession: 138586
A;Acession: 138586
A;Acatus: preliminary; translated from GB/EMBL/DDBJ
A;Acession: L1275 «RES
A;Acession: 1-1275 «RES
A;Cross-references: UNIRROT:Q12881; EMBL:U09116; NID:G483914; PIDN:AAB60345.1; PID:G48391
C;Superfamily: pol polyprotein

Query Match 50.3%; Score 78.5; DB 2; Length 1275; Best Local Similarity 54.8%; Pred. No. 0.012; Matches 17; Conservative 7; Mismatches 6; Indels 1;

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hypothetical prote

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Fri Nov 12 14:55:27 2004

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R;Bernardi, F.;Bernardi, A.
DNA Seq. 1, 147-150, 1990
A;Title: Completed sequence of pKG1800, a vector for determination of transcription termi A;Reference number: S14391; MUID:92190543; PMID:2134186
A;Accession: S14391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
A, Residues: 1-139, 'LIPIPGQ' < BER>
A, Residues: 1-139, 'LIPIPGQ' < BER>
A, Residues: 1-139, 'LIPIPGQ' < BER>
A, Crossa-references: EMBL:X51449, NID:g42412; PIDN:CAA35813.1; PID:g42413
R, Slattner, F.R.; Purblett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: G64811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:P09147; EMBL:X06226; NID:g41522; PIDN:CAA29573.1; PID:g41523 R;Lemaire, H.G.; Mueller-Hill, B. Notleic Adids Res. 14, 7755-771. 1986 A;Title: Nuclectide sequences of the galE gene and the galT gene of E. coli. A;Reference number: S00722; MUID:87040735; PMID:3022232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-338 <BLAT>
Cross-references: GB:AE000178; GB:U00096; NID:g1786967; PIDN:AAC73846.1; PID:g1786974;
Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C90727
UDP-galactose-4-epimerase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: isomerase
A, Pathway: galactose metabolism
C; Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C, Keywords: galactose metabolism; isomerase
F, 3-336/Domain: UDPglucose 4-epimerase homology <UDP>
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H
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C;Species: Escherichia coli
C;Dactes: Dec.1990 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: SQ2089; S00759; S14391; G64811; B25764
R;Lemaire, H.G.
Submitted to the EMBL Data Library, April 1988
A;Reference number: S02089
                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                       UDPglucose 4-epimerase (EC 5.1.3.2) - Escherichia coli (strain K-12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 338,
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nolecule type: DNA
Residues: 1-294,'AFRPTGRTPAKPTVN',310-338 <LEM2>
Cross-references: EMBL:X06226
Note: this sequence has been revised in reference S02089
                                     . 9
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Pred. No. 0.95;
8; Mismatches 5;
Pred. No. 0.017;
                                                                                                                                                   126 APRFIKQVLSDLQRDLDSHTIIMGDFNTPLS 156
                                                                                                     2 APRFIKOILLDLKREIDFNVRLVEYFN-PLS 31
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IKQILLDL-KREIDFNVRLVEYFNPL 30
Best Local Similarity 54.8%; Pro
Matches 17; Conservative 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.8%;
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Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-338 <LEM1>
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Map position: 17 min
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A;Residues: 1-1259 cHAT>
A;Cross-references: UNIPROT:P08547
A;Noce: this sequence was constructed from an alignment of published and unpublished seq
C;Keywords: reverse transcriptase; pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein (LIH 3' region) - human c;Species: Homo sapiens (man) C;Date: 30-Mar-1990 #text_change 09-Jul-2004 C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004 C;Accession: B34087 C;Accession: B34087 B;Schueckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J. A;Title: Origin of the human L1 elements: proposed progenitor genes deduced from a conse A;Reference number: A34087; MUID:88085185; PMID:3692483 A;Accession: B34087 A;Accession: B34087 A;Accession: D34087 A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1275 <DOM>
A;Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AAA51622.1; PID:g3397
C;Superfamily: pol polyprotein
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                                                                                                                                       verse transcriptase homolog - human transposon L1.1
Species: Homo sapiens (man)
Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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Pred. No. 0.012;
7; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1280;
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                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 0
C;Datessaion: 865824
R;Dombroski, B.A.
submitted to the EMBL Data Library, January 1992
A;Description: Isolation of an active human transposable element.
A;Reference number: 865823
A;Status: preliminary
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.7%; Score 77.5; DB 4 ilarity 54.8%; Pred. No. 0.016; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APRFIKOVLSDLORDLDSHTLIMGDFWTPLS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 APRFIKQVLSDLQRDLDSHTIMGDFNTPLS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 APRFIKQILLDLKREIDFNVRLVEYFN-PLS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 APRFIKOILLDLKREIDFNVRLVEYFN-PLS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77.5;
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C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cn 50.3%;
1 Similarity 54.8%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: pol polyprotein
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Best Local Similarity
Matches 17; Conserv
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Matches 17; Conserv
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8 g

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Cypecies: Treptococcus pneumoniae
Cybecies: Streptococcus pneumoniae
Cybecies: Streptococcus pneumoniae
Cybecies: Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
CyAccession: C98054
Rybecies: D.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es
Rybecies: D.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es
Rybecies: D.A.; Alborn Jr., W.; Arnold, J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 200
A; Atthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Rocession: C98054
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: Jas exura
A; Rosses-references: UNIPROT:08DNY6; GB:AE007317; PIDN:AAL00264.1; PID:g15459117; GSPDB:GP
C; Genetics:
                   A;Residues: 1-339 <KUR>
A;Cross-references: UNIBROT:097PK2; GB:AE005672; PIDN:AAK75691.1; PID:g14973098; GSPDB:GRA;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1607
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: UDP-galactose 4-epimerase
(Species: Cyamopsis tetragonoloba (guar, cluster bean)
(Species: Cyamopsis tetragonoloba (guar, cluster bean)
(Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
(Speciesion: T10496
(Species: 10-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
(Species: 142, 147-154, 1999)
(Species: 142, 147-154, 1999)
(A) Title: Isolation and expression of two cDNA clones encoding UDP-galactose epimerase expecies: 1801-1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Status: preliminary; translated from GB/EMBL/DDBJ
A)Anclecule type: mRNA
A)Actiones: 1-354 <BRUS
A)Cross-references: UNIPROT:O65780; EMBL:AJ005081
C)Superferantly: Bescherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C)Steywords: galactose metabolism; isomerase
P;12-350/Domain: UDPglucose 4-epimerase homology <UDP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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                                                                                                                                                                                                                                                                                                                                                DB 2; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
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(2)
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                                                                                                                                                                                                                                                                                                                                      Query Match
37.5%; Score 58.5; Di
Best Local Similarity 38.7%; Pred. No. 1.8;
Matches 12; Conservative 9; Mismatches
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Pred. No. 1.8;
9; Mismatches
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Best Local Similarity 38.7%;
Matches 12; Conservative
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A;Accession: T10496
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Best Local Similarity
Matches 10; Conserva
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C;Superfamily: Escheri
C;Keywords: isomerase
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90727
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res, B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genche A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: prellminary
A;Molecule type: DNA
A;Residuse: 1-338 <HAX>
A;Residuse: 1-338 <HAX>
A;Residuse: 1-338 <HAX>
A;Residuse: 1-338 <HAX>
A;Residuse: 1-3400007; PIDN:BAB34210.1; PID:gl
A;Coresimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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UDP-Galactose-4-epimerase [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Joate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Joate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Joate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Joate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Joate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A.Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A.Accession: D85578
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-338 cSTO-
A.Accession: UNIPROT: QBX942; UNIPROT: QBKJRB; GB: AE005174; NID: G12513688; PIDN: AAG
A.Experimental source: strain O157:H7, substrain EDL933
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B95187
UD-9Jucose 4-epimerase [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95187
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, non, J.D.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
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A;Gene: galE
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%; Score 60.5; DB 2;
46.2%; Pred. No. 0.95;
tive 8; Mismatches 5;
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156 VEQILTDLQKAQPDWSIALLRYFNPV 181
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Best Local Similarity 46.2%
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Length 285; Indels

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UDPGIUCOSE 4-epimerase (BC 5.1.3.2) - Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: 3.7766 Baron, L.S.
J. Bacteriol. 172, 4392-4398, 1990
A;Title: Molecular cloning and physical and functional characterization of the Salmonelle A;Reference number: A37760, MJID:90330544; PMID:2198256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Status: preliminary
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Cross-references: UNIPROT:P22715, GB:M33681, NID:g154046, PIDN:AAA27111.1, PID:g154047
A/Cross-references: UNIPROT:P22715, GB:M3681, NID:g154046, PIDN:AAA27111.1, PID:g154047
C/Superfamily: Bscherichia coli UDPglucose 4-epimerase, UDPglucose 4-epimerase homology
C/Keywords: isomerase
F/3-335/Domain: UDPglucose 4-epimerase homology <UDP>
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36.2%; Score 56.5; DB 1; Length 337;
Best Local Similarity 42.3%; Pred. No. 3.4;
Matches 11; Conservative 9; Mismatches 5; Indels 1
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                          36.5%; Score 57;
45.5%; Pred. No. 3
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156 VEQILTDLQKAQPEWSIALLRYFNPV 181
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141 PRLIGQLITELKKERDLNIHVV 162
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A;Title: The broad bean gene VfNOD32 encodes a nodulin with sequence similarities to chi A;Reference number: Z17436; MUID:96151494; PMID:8587978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-285 <PER>
A;Cross-references: UNIPROT:Q41664; EMBL:Z46911; NID:g1143616; PIDN:CAA87009.1; PID:g114
A;Experimental source: strain Kleine Thueringer
C;Superfamily: alcohol sulfotransferase
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R;Nong, V.; Muentz, K.
submitted to the EMBL Data Library, November 1994
A;Description: A genomic sequence encoding putative narbonin from Vicia sativa.
A;Reference number: S49880
A;Accession: S49898
                                                                                                                                                                         hypothetical narbonin-like 2S protein - fava bean C;Species: Vicia faba (fava bean) C;Species: Vicia faba (fava bean) C;Species: Vicia faba (fava bean) C;Date: 05-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004 C;Accession: $49879 A;Norg, V.; Schlesier, B.; Muentz, K. Submitted to the EMBL Data Library, November 1994 A;Reference number: $49849 A;Reference number: $49849 A;Reference number: $49879 A;Retus: preliminary
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C.Species: Vicia faba (fava bean)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C.Accession: T12157
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C;Species: Vicia sativa (spring vetch, tare)
C;Date: 05-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Mossidus: 1-285 <NON>
A;Cross-references: UNIPROT:Q41704; EMBL:Z46835; NID:g600112; PID:g600113
C;Superfamily: alcohol sulfotransferase
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A;Residues: 1-285 «NON»
A;Cross-references: UNIPROT:Q41660; EMBL:Z46826; NID:g600101; PID:g600102
C;Superfamily: alcohol sulfotransferase
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A,Molecule type: mRNA
141 PRLIGOLITELKKERDLNIHVV 162
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein November 10, 2004, 12:27:34 ; Search time 37.8532 Seconds (without alignments) 471.205 Million cell updates/sec Run on:

US-10-092-750-43 156 1 RAPRFIKQILLDLKREIDFNVRLVEYFNPLS 31

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched: 1825181 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Q7kz41 homo sapien	0 homo sa	O00362 homo sapien	O00363 homo sapien	O00366 homo sapien	homo	000370 homo sapien	O00375 homo sapien	O00378 homo sapien	homo	homod	77 hon	P08547 homo sapien	Q6znc3 homo sapien	52 hor	homod	000372 homo sapien	Q6znd9 homo sapien	6 hor	Q6zne0 homo sapien	Bad18435 homo sapi	Q8naq0 homo sapien		Ŋ	escheri			Q8fjr9 escherichia	escherich	Q83sa4 shigella fl	_
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* 2	Match				50.3				50.3	50.3	50.3	50.0	50.0	49.7	48.4	48.4	47.8		•	45.8	45.2	45.2	42.0	œ	œ.	œ,	œ.	œ,	38.8	œ	38.8	
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Q7rj94 plasmodium Q6d7d6 erwinia car	Q8dny6 streptococc	Q97pk2 streptococc	O65780 cyamopsis t	Q41660 vicia faba	Q41664 vicia faba	Q41704 vicia sativ	030775 helicobacte	Q7f9h2 oryza sativ	Cae05576 oryza sat		P22715 salmonella	062107 caenorhabdi
Q7RJ94 O6D7D6	QBDNY6	Q97PK2	GAE1 CYATE	Q41660	Q41664	Q41704	030775	Q7F9H2	CAE05576	GALE SALTI	GALE SALTY	062107
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339	339	339	354	285	285	285	344	701	701	338	338	347
37.8	37.5	37.5	36.9	36.5	36.5	36.5	36.5	36.5	36.5	36.2	36.2	36.2
		'n	'n	57	57	57	57	57	57	رى	6.5	3
58.5	58.5	58.	57.5							5	56	56

## ALIGNMENTS

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[1] — SEQUENCE FROM N.A. MEDLINE=89233117; PubMed=2497061; MeDLINE=89233117; PubMed=2497061; Mode-Samuels P., Wong C., Mathias S.L., Scott A.F., Kazazian H.H. Jr., Antonarakis S.E.; "Characterization of a nondeleterious L1 insertion in an intron of the human factor VIII gene and further evidence of open reading frames in functional L1 elements."; Genomics 4:290-296(1989).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Momo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Woods-Samuels P.; Submitted (APR-1989) to the EMBL/GenBank/DDBJ databases.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                     C.J. 2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein (Fragment) Homo sapiens (Human).
                                                                          PRT; 1192 AA
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InterPro; IPR005135; Exc_endo_phos.
InterPro; IPR000477; RVTse.
Pfam; PP03372; Exc_endo_phos; 1.
Pfam; PP00078; RVT; I.
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                                                                               MEDLINE=97285120; PubMed=9140393;
A Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
A Deberardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
A Deberardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
I. Mat. Genet. 16:37-43(1997).
I. Mat. Genet. 16:37-43(1997).
R. EMBL, U93563; AAG71261.1;
R. PIR, S28096; B28096.
R. PIR, S28650; S23650.
R. GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA directed DNA polymerase activity; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
R. InterPro; IPR006135; Exo_endo_phos.
R. InterPro; IPR006477; RVTSe.
R. Pfam; PF03372; Exo_endo_phos; I.R. Pfam; PF0372; Exo_endo_phos; I.R. Pfam; PF0377; RVTSe.
R. Prosing R. R. Prosing R. R. Prosing R. R. Pfam; PF0377; RVTSe.
R. Pfam; PF0377; Exo_endo_phos; I.R. Pfam; PF0377; RVTSe.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-directed DNA polymerase, Transferase.
SEQUENCE 1275 AA; 149062 MW; 350B4F0358E525F0 CRC64;
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SEQUENCE 1275 AA; 149201 MW; 23D516D6E4358F28 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pfam; PF00078; RVT; 1.
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Matches 17; Conservative
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Homo sapiens (Human)
                                                              SEQUENCE FROM N.A.
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es 17; Conserv
      NCBI_TaxID=9606;
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RESULT 4

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MEDLINE=97285120; PubMed=9140393;
Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
Sassaman D.M., Dombroski B.A., Swergold G.D., Kazazian H.H. Jr.;
DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
"Many human Li elements are capable of retrotransposition.";
Nat. Genet. 16.37-43(1997).
Nat. Genet. 16.37-43(1997).
PIRI, B28096; B28096.
PIR, S23650; S23650.
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                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
InterPro; IPRO06135; Exc. endo_phos.
InterPro; IPRO06477; RVTSe.
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Pfam; PF00078; RVT; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149033 MW; 07E98F8F4DB831A2 CRC64;
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SEQUENCE 1275 AA; 149007 MW; A866976EA3FD8F74 CRC64;
000363;
01-JUD-1997 (TrEMBLrel. 04, Created)
01-JUD-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pfam; PF03372; Exo endo phos; 1.
Pfam; PF00078; RVT; 1.
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les 17; Conservative
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Best Local Similarity
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MEDLINE=97285120; PubMed=9140393;
Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                            50.3%; Score 78.5; DB 2; Length 1275; 54.8%; Pred. No. 0.032; ive 7; Mismatches 6; Indels 1.
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                                                     Pfam; PF03372; Exo_endo_phos; 1.
Pfam; PF0078; RVT; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149010 MW; 588703688E7129FF CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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54.8%; Pred. No. 0.03
:ive 7; Mismatches
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01-JUL-1997 (TrEMBLrel. 04, Last seqn
01-MAR-2004 (TrEMBLrel. 26, Last anno
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IPR005135; Exo endo phos. IPR000477; RVTSe.
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Matches 17; Conservative
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Matches 17; Conservative
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  InterPro;
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Nat. Genet. 16:37-43(1997).

PEMBL, U93569; AAC51271.1; -.

PIR, B28096; B28096.

PIR, S23650, S23650.

GO, GO:000378; F:RNA binding; IEA.

GO, GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO, GO:0006278; P:RNA-dependent DNA replication; IEA.
     Gaps
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
VCBI_TaxID=9606;
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Homo sapiens (Human).

Homo sapiens (Human).

Bukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryotes, Metazoa; Chordates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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  Indels
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Pfam; PF00078; RVT; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149077 MW; 3BBC3B2DC2E06B61 CRC64;
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                                                     2 APRFIKQILLDLKREIDFNVRLVEYFN-PLS 31
7; Mismatches
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17; Conservative
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MEDLINE=21668188; PubMed=11810275;
Benjes S.M., Morris C.M.;
"A full-length and potentially active LINE element is integrated
polymorphically within the IGL locus in a genomically unstable region
of chromosome 22.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pfam; PF00378; RVT; 1.
Hypothetical protein; RN4-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149009 MW; B327D9D50A581764 CRC64;
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EMBL, AF421375; AAL50637.1; -.

EMBL, AF421375; AAL50637.1; -.

PIR; B28065; B28096.

PIR; S23660; S23650.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0006278; P:RNA-dependent DNA replication; IEA.

InterPro; IPR000477; RVTSG.
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Pfam; PF00078; RVT; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 148879 NW; F006F74BBBB72B87 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 54.8
Matches 17; Conservative
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Homo sapiens (Human).
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                                                             RRA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA BER RA B
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                                                                                                                                                                                                                                                                                                    Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita Matsuo K., Nakamura Y., Sehine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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53.6%; Pred. No. 0.0064;
tive 7; Mismatches 6; Indels
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"NEDO human cDNA sequencing project.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AKI313; BAD18477.1;
SEQUENCE 244 AA; 28032 MW; 0B7AD3D0357935BI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AKCI31313, BAD18477.1;
INTERPRO, IPRO05135, Exo endo phos.
Pfam. PF03372; Exo-endo phos; 1.
SEQUENCE 244 AA; 28032 MW; 0B7AD3D0357935B1 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update) co-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypotherical protein FLJ16301. Homo sapiens (Human).
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12-MAX-2004 (TrEMBirel. 27, Created)
12-MAX-2004 (TrEMBirel. 27, Last sequence update)
2-MAX-2004 (TrEMBirel. 27, Last annotation update)
CDNA FL16301 fis, clone PLACE7000333.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=9606;
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LINI_HUMAN
ID _LINI_HUMAN
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PRT; 1259 AA.

STANDARD;

244 AA.

Q6ZN98; 05-JUL-2004 (TrEMBLrel. 27, Created)

PRELIMINARY;

86NZ90

314 AA

PRT;

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TISSUB-TORGUE;

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ono Y., Hotuta T., Watanabe M.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishi S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (Mar-2004) to the EMBL/GenBank/DDBJ databases.

BMBL, AK131275; BADJ8452.1;
NON_TER 314
                                                                                                                                                                                                   12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
CDNA PLJ16220 fis, clone CTONG3002552. (Fragment).
How sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                           RESULT 15
                                                                                      BAD18452
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TISSUB-Tongue;

A manai H., Watanabe S., Ishida S., Ono Y., Horuta T., Watanabe M.,

A Tanai H., Watanabe S., Ishida S., Ono Y., Horuta T., Watanabe M.,

Sugiyama T., Irie R., Otsuki T., Sato H., Wakamarsu A., Ishii S.,

Yamamoto J., Isono Y., Kawai-Hio Y., Sato R., Nishikawa T.,

Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

EMBL; AK131275; BAD18452.1; ---

RIL Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases.

RIL Submitted (WAR-2004) To the EMBL/GenBank/DDBJ databases.

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE AK131275; BAD18452.1; ---

RIL SERIE
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL1016220.

Hypothetical protein FL1016220.

Bukano sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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49.7%; Score 77.5; DB 1; Length 1259;
Best Local Similarity 54.8%; Pred. No. 0.044;
Matches 17; Conservative 7; Mismatches 6; Indels 1
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48.4%; Score 75.5; DB 2; Length 314;
Best Local Similarity 51.6%; Pred. No. 0.019;
Matches 16; Conservative 8; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03372; Exo_endo_phos; 1.
Pfam; PF00078; RVT; 1.
Direct protein sequencing; RNA-directed DNA polymerase.
SEQUENCE 1259 AA: 147112 NW; F3EC18A3803919F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA; 36311 MW; 2C37DD7DD1001A56 CRC64;
                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Homo sapiens (Human).
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Query Match

48.4%; Score 75.5; DB 2; Length 314;
Best Local Similarity 51.6%; Pred. No. 0.019;
Matches 16; Conservative 9; Mismatches 6; Indels 1
SEQUENCE 314 AA; 36311 MW; 2C37DD7DD1001A56 CRC64;
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Sequence 3, Application US/09428517
Patent No. 6251636
Patent No. 6251636
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
TITLE REFERENCE: 30062-2005-00
CURRENT APPLICATION UNDER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
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Query Match
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Sequence 3, Appli
Sequence 82, Appli
Sequence 82, Appl
Sequence 5390, Appl
Sequence 5375, Appl
Sequence 23751, Appl
Sequence 16, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
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Sequence 29, Appl
Sequence 19, Appl
Sequence 5421, Appl
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Sequence 23, Appl
Sequence 26, Appl
Sequence 46, Appl
Sequence 19, Appl
Sequence 729, Appl
Sequence 2584, A
Sequence 2594, A
Sequence 27619, Appl
                                                                       November 10, 2004, 13:44:14 ; Search time 9.51698 Seconds (without alignments) 181.178 Million cell updates/sec
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Sequence 3
Sequence 5
Sequence 5
Sequence 8
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-26051
US-09-544-664B-46
US-09-544-664B-46
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US-09-5252-991A-25984
US-09-252-991A-27619
US-09-199-637A-130
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                                                                                                                 US-10-092-750-44
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1 IVAIIAGRLRMLGDQFNGELEASAKN 26
                                                                                                                                                                                         478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match 1
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Sequence 4, Application US/09428517

Sequence 4, Application US/09428517

Sequence 4, Application US/09428517

Sequence 4, Application US/09428517

APPLICANT: Betlach, Mary C.

APPLICANT: Ban, Sanjay Krishnakant

APPLICANT: Application Webert

APPLICANT: McDaniel, Robert

APPLICANT: McDaniel, Robert

APPLICANT: McDaniel, Robert

APPLICANT: McDaniel, Robert

CURRENT APPLICATION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 30062-20029.00

CURRENT PILING DATE: 1999-10-28

EARLIER FILING DATE: 1999-10-28

EARLIER PILING DATE: 1999-10-28

SALIER PILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

ERRORD: Patentin Ver. 2.1

FUNDET: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: 
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VGGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant
OTHER INFORMATION: Oleandolide PKS
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US-09-715-834-2
US-09-270-767-47579
US-09-270-76-33163
US-09-328-352-5770
US-09-318-328-3770
US-09-252-991A-21011
US-09-252-991A-24030
US-09-252-991A-24030
US-09-252-991A-24030
US-09-252-991A-24030
US-09-252-991A-24030
US-09-252-991A-24030
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40.0%; Pred. No. 19;
tive 8; Mismatches
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Patent No. 6309820
GENERAL INFORMATION:
SPREAS, Andrew B.
APPLICANT: SPREAS, Andrew B.
APPLICANT: FOWLKES, Dana M.
APPLICANT: KAY, Brian K.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Betlach, Mary C.

APPLICANT: Betlach, Mary C.

APPLICANT: Mobaniel, Robert

APPLICANT: And, Li

TILE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

TILE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REPERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT APPLICATION NUMBER: 60/120,254

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER APPLICATION NUMBER: 60/106,100

EARLIER PILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 2

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39.2%; Score 49; DB 3; Length 4150;
Best Local Similarity 36.0%; Pred. No. 74;
Matches 9; Conservative 9; Mismatches 7; Indels
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER PRILING DATE: 1998-10-29
; EARLIER PILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SCGTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3816
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; Sequence 2, Application US/09428517
; Patent No. 6251636
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-630-915A-82
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APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. 6709821h
KAY, Brian K.
FOWLKES, Dana M.
MCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CORREST: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USS
CONTRY: USS
CONTRY: USS
CONTRY: USS
COMPUTER: Floppy disk
COMPUTER: 13 PP C COMPALIDE
OPERATING SYSTEM: PC COMPALIDE
OPERATING SYSTEM: PC COMPALIDE
OPERATION DATE: 13-Jun-2001
FILING DATE: 13-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                              SIREDI NEW YORK
COUNTRY: New YORK
COUNTRY: OBS-2711
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION NUMBER: US/08/630,915A
FILING DATE: DESLIE
REGISTRATION NUMBER: 13,872
RETERENCE/DOCKET NUMBER: 110.1-74
TELEBHONE: (212) 790-9909
TELEFA: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE THRACTERISTICS:
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ņ,
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TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STAIE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/09879957
Patent No. 6709821
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-82
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Query Match
Best Local Similarity
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Patent No. 6617156

Patent No. MATTON:

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BUTERC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BUTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMERR: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6612

SOFTWARE: Patentin version 3.1

SEQ ID NO 5390

LENGTH: 351
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.6%; Score 44.5; DB 4; Length 40; 57.9%; Pred. No. 1.6; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHRACATERISTICS:
TENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.6%; Score 44.5; I Best Local Similarity 40.7%; Pred. No. 22; Matches 11; Conservative 6; Mismatches
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 82:

S2-09-879-957-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVAIIAGRIRML---GDOFNGELEASA 24
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PRIOR APPLICATION NUMBER: US 60/055,778
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Patent No. 6617156
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 RLRMLGDOFNGELEASAKN 26
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21 KLRVLGYNHNGE-EAQTKN 38
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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Best Local Similarity
Matches 11; Conserva
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US-09-134-000C-5975
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US-09-134-000C-5390
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Sequence 27945, Application US/09252991A

Sequence 27945, Application US/09252991A

Sequence 27945, Application US/09252991A

Patent No. 651795

GENERAL INFORMATION:

APPLICANT: Marc J. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107796.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 315
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Sequence 23751, Application US/09252991A

Sequence 23751, Application US/09252991A

Sequence 23751, Application US/09252991A

Tattacon Invention: Raced Acid Acid And Amino Acid Sequences Relating to Pseudomonas

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 415
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                                                                                                                                                                                                                                                            Query Match 35.2%; Score 44; DB 4; Length 268; Best Local Similarity 50.0%; Pred. No. 19; Matches 11; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4;
Pred. No. 33;
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91 LVYVIDGRLRVSDGQETHELEA 112
                                                                                                                                                                                                                                                                                                                                                                                      1 IVAIIAGRLRMLGDQFNGELEA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                  TYPE: PRT ORGANISM: Enterococcus faecalis
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5975
LENGTH: 268
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US-09-252-991A-23751
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Gaps ., H

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34.8%; Score 43.5; DB 1; Length 54; 55.0%; Pred. No. 3.4; tive 2; Mismatches 6; Indels
REFERENCE/DOCKET NUMBER: 7683-062
TELECOMONINICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           8 RLRMLGDQFNGE-LEASAKN 26
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20 KLRVLGYNHNGEWCEAQTKN 39
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                                                  TELERAX: (212, 000)
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TVPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERICTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-167-035-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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US-08-208-887A-28
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APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Margolis, Benjamin L.

TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EURARYOTIC TYROSINE
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
    Gaps
                                                                                                                                                                                       Sequence 16, Application US/09023905A

Patent No. 647570

Gequence 16, Application US/09023905A

Patent No. 647570

Geptence No. 647570

APPLICANT: Roberts, Thomas M.

APPLICANT: King, Frederick J.

APPLICANT: Harris, David F.

APPLICANT: Harris, David F.

APPLICANT: Harris, David F.

APPLICANT: Harris, David F.

APPLICANT: Harris, David F.

APPLICANT: Harris, David F.

TILE OF INVENTION: Differentiation Enhancing Factors and Uses

TILE OF INVENTION: Differentiation Enhancing Factors

TILE OF INVENTION: Differentiation Enhancing Factors

TILE OF INVENTION: DAVIBER: US/09/023,905A

CURRENT FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-14

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: 7-LOPPY disk
COMPUTER: 1BM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,035
    10;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1993
16-DEC-1993
18-DEC-1993
18-DEC-1993
                                                                                         142 VALLRGRORPLHDHFGGRRDHRA 164
                                           2 VAIIAGRLRMLGDQFNGELEASA 24
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US-08-167-035-28
; Sequence 28, Application US/08167035
; Parent No. 5618691
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  3;
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NAME: CORUZZI, DAURA A.
REGISTRATION NUMBER: 30,742
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-023-905A-16
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Best Local Similarity
Matches 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                  US-09-023-905A-16
Matches
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Sequence 28, Application US/08208887A

Sequence 28, Application US/08208887A

Patent No. 567421

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 51
CORRESSONDENCE ADDRESSS:
CORRESSONDENCE ADDRESSS:
STREET: 1155 Avenue of the Americas
COTTY: New York
COTTY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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Pred. No. 3.4;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, Laura A.
REFERENCE/DOCKET NUMBER: 7683-063
TELECOMMUNICATION INFORMATION:
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Gaps

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Sequence 30, Application US/09280598
Patent No. 6391584
GENERAL INFORMATION:
Patent No. 6391584
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlis, Edward Y.
APPLICANT: Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applica
SEQ ID NO 19
LENGTH: 54
TYPE: PRT
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAMME/KEY: Domain
OTHER INFORMATION: amino acid sequence of C-Abl SH3 domain
US-09-346-510B-19
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: ELOPPY disk
COMPUTER: EL PR PC compatible
COMPUTER: EL PR PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
SOFTWARE: PATENTIN Release #1.0, Version #1.25
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55.0%; Pred. No. 3.4;
iive 2; Mismatches 6;
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34.8%; Score 43.5; Di
Best Local Similarity 55.0%; Pred. No. 3.4;
Matches 11; Conservative 2; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/252,820
FILING DATE: 02-UUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 54 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RLRMLGDQFNGE-LEASAKN 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 KLRVLGYNHNGEWCEAQTKN 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-280-598-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-280-598-30
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                                                                                                                                                                                                                                  APPLICANT: Schlessinger, Joseph
APPLICANT: Schlick, Edward Y
APPLICANT: Schlick, Edward Y
APPLICANT: Schlick, Edward Y
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
TITLE OF INVENTION: DENTIFYING TARGET PROTEINS
FOR INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTY: 10036-2711
ZIP: 10036-2711
ZIP: TO036-2711
ZIP: TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
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Patent No. 6881014
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR PILITALION NUMBER: 08/871,732
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                          Sequence 28, Application US/08539005
Patent No. 5858686
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 RLRMLGDQFNGE-LEASAKN 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELERAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                           US-08-539-005-28
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Search completed: November 10, 2004, 14:55:33 Job time : 9.56698 secs

us-10-092-750-44.rai

Sequence 92, Appl Sequence 226, App Sequence 228, App Sequence 251, App Sequence 252, App Sequence 252, App Sequence 244, App Sequence 244, Appl Sequence 244, Appl Sequence 279915, Sequence 279915, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, Sequence 218650, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 61870, A Sequence 11868, Sequence 11868, Sequence 11868, Sequence 11868, Sequence 11878, A Sequence 55946, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 11878, A Sequence 1

OM protein

Run on:

Sequence:

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Sequence 40. 4 Application US/10092750

Sequence 40. Application US/10092750

Publication No. US2003003157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: HATGHT, Martin C.

TITLE OF INVENTION: Polypeptides Interactive with BCL-XI

FILE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

CURRENT FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 44

LEAGTH: 26

LEAGTH: 26

LEAGTH: 26

LEAGTH: 26

LYPE: PRINCE HATCH CAPPERINGE

US-10-092-750-44
100.0%; Score 125; DB 14;
100.0%; Pred. No. 3.1e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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; Sequence 238718
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%
Best Local Similarity 100.0%
Matches 26; Conservative
  RESULT 1
US-10-092-750-44
  8
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Sequence 238718,
                                                                                   November 11, 2004, 01:28:30; Search time 30.0717 Seconds (without alignments) 305.399 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/Der_Maw PuBh.pepp:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUBh.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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17 US-10-425-115-238718
18 US-09-925-300-1530
15 US-10-307-817-90
15 US-10-287-226-230
15 US-10-287-226-230
15 US-10-287-226-232
15 US-10-287-226-232
15 US-10-287-226-246
15 US-10-287-226-246
15 US-10-287-226-246
15 US-10-287-226-246
15 US-10-307-817-86
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                                                                                                                                                                                                                              1566620 segs, 353225886 residues
                                                                                                                                     US-10-092-750-44
125
1 IVAIIAGRLRMLGDQFNGELEASAKN 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB ID
                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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10072
10091
10091
10095
110095
11000
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Perfect score:
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Database :

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Gaps

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Indels

Length 26;

Result

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APPLICANT:
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us-10-0

. APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

TITLE OF INVESTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVESTION: Plants

FILE REPERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 238718

LENGTH: 71

TURN THE TENT APPLICATION NUMBER: US/10/425,115

THE TENT APPLICATION NUMBER: US/10/425,115

THE TENT APPLICATION NUMBER: US/10/425,115

THE TENT APPLICATION NUMBER: US/10/425,115

THE TENT APPLICATION NUMBER: US/10/425,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (178)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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| Patent No. US20202151681A1
| Patent No. US202020151681A1
| GAPPLICANT: Craig Rosen,
| APPLICANT: Steve Ruben
| ITTLE OF INVENTION NUCLEIC Acids, Proteins and Antibodies
| FILE REPERENCE: PA101
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT PILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05988
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 88; DB 17; Length 71; 89.5%; Pred. No. 1.2e-06; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.6%; Score 52; DB 9; Length 363; 40.0%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Clone ID: MRT4577_14929C.1.pep
US-10-425-115-238718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
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182 LVSSLTSGLLTIGDRFGGALDAAAK 206
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, Sequence 90, Application US/10307817
, Publication No. US20040058338A1
, GENERAL INFORMATION:
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Best Local Similarity 89.5'
Matches 17; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1530
LENGTH: 363
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ORGANISM: Homo sapiens
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
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Gaps
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PEPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
                                                                                                                                                                                                                                                                                         .;
0
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                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                             ; Score 52; DB 1
; Pred. No. 24;
7; Mismatches
FILE REFERENCE: 21402-502C
CURRENT PEDILGATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 90
LENGTH: 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
                                                                                                                                                                                                                                                                                                                                                                                891 LVSSLTSGLLTIGDRFGGALDAAAK 915
                                                                                                                                                                                                                                                                                                                                    1 IVALIAGRIRMLGDOFNGELEASAK 25
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Rothenberg, Mark E.,
Shenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jir., Raymond J.,
Vernet, Corine A.M.,
Zerhusen, Bryan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/334, 421
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/364,392
PRIOR FILING DATE: 2002-02-04
PRIOR PELLING DATE: 2002-02-07
PRIOR PAPLICATION NUMBER: 60/360,148
PRIOR PLILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/364,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 230, Application US/10287226
Publication No. US20040086875A1
BAPPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burges, Catherine E.,
Chant, John S.,
Chaudhuri, Amitabha,
Dibippo, Vincent A.,
Edinger, Shlomit R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li, Li,
Malyankar, Uriel M.,
Macbougall, John R.,
Mezes, Peter S.,
Miller, Charles E.,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
Khramtsov, Nikolai,
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0%;
Matches 10; Conservative
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Gangolli, Esha A.,
Gorman, Linda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan, Meera,
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Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isen, Andrew,
                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-307-817-90
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APPLICANT: Zernug, Mei styan D.,
APPLICANT: Zernug, Mei styan D.,
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE REPERBRES: 21402-480C
CURRENT APPLICATION NUMBER: 00/334,421
PRIOR PELICATION NUMBER: 60/334,421
PRIOR PLICATION NUMBER: 60/334,421
PRIOR PLICATION NUMBER: 60/334,421
PRIOR PLICATION NUMBER: 60/336,148
PRIOR PLILING DATE: 2002-02-04
PRIOR PLILING DATE: 2002-02-07
PRIOR PLILING DATE: 2002-02-07
PRIOR PLILING DATE: 2002-03-13
PRIOR PLILING DATE: 2002-03-13
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41.6%; Score 52; DB 15; Length 1091;
Best Local Similarity 40.0%; Pred. No. 24;
Matches 10; Conservative 7; Mismatches 8; Indels
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Rothenberg, Mark E.,
Shenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Ur., Raymond J.,
Vernet, Corine A.M.,
Zerhusen, Bryan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-307-817-86; Sequence 86, Application US/10307817; Publication No. US20040058338A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ort, Tatiana,
Padigaru, Muralidhara
                                                                                                                                                                                                                                                Li, Li,
Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Miller, Isabelle,
                                                                                                             Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
Khramtsov, Nikolai,
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Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-287-226-669
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PRIOR FILING DATE: 2002-03-13

PRIOR PELING DATE: 2002-08-20

PRIOR PELING DATE: 2002-08-20

PRIOR PILING DATE: 2002-08-20

PRIOR PILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 60/334,526

PRIOR PELING DATE: 2002-03-13

PRIOR PELING DATE: 2002-03-13

PRIOR PELING DATE: 2002-03-13

PRIOR PELING DATE: 2001-11-28

PRIOR PELING DATE: 2001-11-28

PRIOR PELING DATE: 2001-11-28

PRIOR PELING DATE: 2001-11-28

PRIOR PELING DATE: 2001-11-28

PRIOR PELING DATE: 2001-11-20

PRIOR PELING DATE: 2001-11-20

PROBATE: 2001-11-20
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US-10-307-817-469

is Sequence 469, Application US/10307817

j Publication No. US20040058338A1

is GENERAL INFORMATION: MORE PROTEINS AND NUCLEIC ACIDS ENCODING SAME

j TITLE OF INVENTION: NOWHER: US/10/307,817

is CURRENT APPLICATION NUMBER: US/10/307,817

is CURRENT FILING DATE: 2002-12-02

is NUMBER OF SEQ ID NOS: 682

is SEQ ID NO 469

is SEQ ID NO 469

is LENGTH: 1091
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41.6%; Score 52; DB 15; Length 1091;
Best Local Similarity 40.0%; Pred. No. 24;
Matches 10; Conservative 7; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
41.6%; Score 52; DB 15; Length 1072;
Best Local Similarity 40.0%; Pred. No. 24;
Matches 10; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891 LVSSLTSGLLTIGDRFGGALDAAAK 915
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Publication No. US20040086875A1
GENERAL INFORMATION:
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APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Essen, Andrew,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-226-230
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APPLICANT:
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APPLICANT:
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             APPLICANT: Age et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILLE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSequist version 0.1
LENGTH: 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
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CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,392
PRIOR FILING DATE: 2002-02-04
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Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Spenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
Vernet, Corine A.,
Vernet, Corine A.M.,
Zerhusen, Bryan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 232, Application US/10287226 Publication No. US20040086875A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ages, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boddog, Ference,
APPLICANT: Chaut, John S.,
APPLICANT: Chauth John S.,
APPLICANT: Chauth John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Li,
Malyankar, Uriel M.,
MacDougall, John R.,
Macse, Peter S.
Miller, Charles E.,
Miller, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Padigaru, Muralidhara,
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Ellerman, Karen,
Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
Ji, Weizhen,
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Khramtsov, Nikolai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chean Eng,
                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-307-817-86
GENERAL INFORMATION:
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US-10-287-226-232
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/360,148
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-13
PRIOR PLING DATE: 2002-08-20
PRIOR PLING DATE: 2002-08-20
PRIOR PLING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-13
PRIOR PLING DATE: 2001-11-28
PRIOR PLING DATE: 2001-11-28
PRIOR PLING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238, Application US/10287226 Publication No. US20040086875A1 GENERAL INFORMATION:
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APPLICANT: Alsobrook, John P.,
APPLICANT: Bergha, Constance,
APPLICANT: Bergha, Constance,
APPLICANT: Chauf, John S.,
APPLICANT: Chauf, John S.,
APPLICANT: Chauf, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Edinger, Shlomit R.,
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Malyankar, Uriel M.,
MacDougall, John R.,
Mares, Peter S.
Miller, Charles E.,
Miller, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Padigaru, Muralidhara
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Ji, Weizhen,
Kekuda, Ramesh,
Khramtsov, Nikolai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patturajan, Meera,
Rastelli, Luca,
Rieger, Daniel K.,
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Shenoy, Suresh G.,
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Gangolli, Esha A.,
Gorman, Linda,
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Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isen, Andrew,
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ORGANISM: Homo sapiens
US-10-287-226-232
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APPLICANT: Spaderna, Streen G.,
APPLICANT: Spaderna, Streen K.,
APPLICANT: Spaderna, Streen K.,
APPLICANT: Spaderna, Streen K.,
APPLICANT: Spaderna, Jr., Raymond J.,
APPLICANT: Carinsen, Bryan D.,
APPLICANT: Carinsen, Bryan D.,
APPLICANT: Zhong, Mei, Bryan D.,
APPLICANT: Zhong, Mei, Bryan D.,
APPLICANT: Zhong, Mei, Bryan D.,
APPLICANT: Zhong, Mei, Bryan D.,
APPLICANT: Schong, Mei, Bryan D.,
APPLICANTON NUMBER: 60/334,421
PRIOR APPLICATION NUMBER: 60/334,000
PRIOR PILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/344,000
PRIOR APPLICATION NUMBER: 60/344,000
PRIOR APPLICATION NUMBER: 60/344,409
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-11-30
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Publication No. US20040086875A1
GENERAL INFORMATION:
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APPLICANT: Alebrook, John P.,
APPLICANT: Berghe, Contance,
APPLICANT: Berghe, Contance,
APPLICANT: Chant, John S.,
APPLICANT: Chant, John S.,
APPLICANT: Chanthuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Esten, Andrew,
APPLICANT: Elsen, Andrew,
APPLICANT: Elsen, Andrew,
APPLICANT: Gangolli, Esha A.,
                                                                               adigaru, Muralidhara,
                                                                                                                                                                                        Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                                                     Patturajan, Meera,
Rastelli, Luca,
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ORGANISM: Homo sapiens
US-10-287-226-246
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US-10-287-226-668
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                    APPLICANT: Zerbusen, Biryan D.,
APPLICANT: Zerbusen, Biryan D.,
APPLICANT: Zerbusen, Biryan D.,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT APPLICATION NUMBER: US/034,421
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/344,409
PRIOR PILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR PILING DATE: 2002-03-03
PRIOR PILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR PILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR PILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/334,527
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334,027
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PRIOR APPLICATION NUMBER: 60/334,027
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NUMBER OF SEQ ID NOS: 673
SOWTWARE: CuraSequist version 0.1
SEQ ID NO 238
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APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Millet, Isabelle,
Vernet, Corine A.M.,
Zerhusen, Bryan D.,
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Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
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ORGANISM: Homo sapiens
US-10-287-226-238
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Gangolli,
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TTTLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TTTLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-4806
CURRENT APPLICATION NUMBER: 60/334,421
PRIOR PAPLICATION NUMBER: 60/354,392
PRIOR PAPLICATION NUMBER: 60/354,392
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR FILING DATE: 2002-02-77
PRIOR APPLICATION NUMBER: 60/404,821
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/404,821
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR PILING DATE: 2002-11-30
PRIOR PILING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-13
PRIOR PILING DATE: 2001-11-28
PRIOR PILING DATE: 2001-11-28
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41.6%; Score 52; DB 15; Length 1100;
Best Local Similarity 40.0%; Pred, No. 24;
Matches 10; Conservative 7; Mismatches 8; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
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Publication No. US20040058338A1
GENERAL INFORMATION:
APPLICANT: Agee et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rastellí, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                                                      Li, Li, Mayyankar, Uriel M., MacDougall, John R., Mazes, Peter S. Miller, Charles E., Miller, Isabelle, Oot, Chean Eng, Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                       Padigaru, Muralidhara
                                                                                         Khramtsov, Nikolai,
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Valerie,
Gerlach, Valerie
Ji, Weizhen,
Kekuda, Ramesh,
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US-10-287-226-668
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US-10-307-817-84
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SEQ ID NO 668
LENGTH: 1100
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RESULT 14
US-10-307-817-92

i Sequence 92, Application US/10307817
i Publication No. US20040058338A1
i GENERAL INFORMATION:
i APPLICANT: Agee et al.
i TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
i TITLE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT PILLING DATE: 2002-12-02
i SOFTWARE: CuraSeqList version 0.1
i SEQ ID NO 92
i LENGTH: 1101
i TYPE: PRT
coranism: Homo sapiens
uS-10-307-817-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-502C CURRENT APPLICATION NUMBER: US/10/307,817 CURRENT FILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 682 SOFTWARE: CuraSeqList version 0.1 SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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40.0%; Pred. No. 24;
tive 7; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 41.6%; Score 52; DB 15; Length 1101; Best Local Similarity 40.0%; Pred. No. 24; Msmatches 8; Indels Castches 10; Conservative 7; Mismatches 8; Indels C
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920 LVSSLTSGLLTIGDRFGGALDAAAK 944
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920 LVSSLTSGLLTIGDRFGGALDAAAK 944
                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVAIIAGRLRMLGDQFNGELEASAK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaut, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Chique, Yincent A.,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Eisen, Andrew,
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Malyankar, Uriel M.,
MacDougall, John R.,
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Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
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angolli, Esha A.,
                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                     ; LENGTH: 1101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-84
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APPLICANT: Miller, Isaballe,
APPLICANT: Miller, Isaballe,
APPLICANT: Ooi, Charles B.,
APPLICANT: Ooi, Charles B.,
APPLICANT: Ooi, Chen Brag,
APPLICANT: Ooi, Chen Brag,
APPLICANT: Ooi, Chen Brag,
APPLICANT: Padigatur, Muralidhara,
APPLICANT: Rieger, Daniel K.,
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APPLICANT: Respective, Muralidhara,
APPLICANT: Rieger, Daniel K.,
APPLICANT: Respective, Muralidhara,
APPLICANT: Repert, Colled K.,
APPLICANT: Taupler, Colled K.,
APPLICANT: Taupler, Chen Brag,
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GenCore version 5.1.6
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- protein search, using sw model OM protein

November 10, 2004, 13:40:53 ; Search time 6.37736 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-44 125 1 IVAIIAGRLRMLGDQFNGELEASAKN 26 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:\*
1: Dirl:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	citrate (pro-		polyketide synthas	Н	hypothetical prote	prophage pi3 prote	prophage pil prote	isoamylase (EC 3.2	polyamine-binding	hypothetical prote	hypothetical prote	lysR-family transc	protein F3M18.12 [	hemagglutinin/hemo	phosphatase (RapE)	hypothetical BCR/A	hypothetical prote	thiamin biosynthes	hypothetical prote	NN8-4AG - human (f	serine-type D-Ala-	conserved hypothet	hypothetical prote	1 prot	hypothetical prote	ы	protein-tyrosine k		
SUMMARIES	. QI	A35007	S21173	S43048	T02574	H75111	C86800	B86683		AC2436	H71021		AB0431	F86410	H81193	B69677	151936	D83858	E83599	AD3198	G02453	A64117	m	E98197	T18713	49	S62562	17	C24773	-
	DB	7	~	7	~	N	N	N	~	N	Н	~	~1	~	7	N	4	7	7	N	~	7	~	0	7	~1	N	N	N	Ŋ
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ф	Query Match	1 -1	н	-1	$\boldsymbol{\sigma}$	α	~	r	r	o	φ	Φ	ω	36.0	w	T()	L >	п)	R.	LL3	w	T()	w	เม	(U)	ഗ	S.	4,	44	4
	Score	52	25	52	49	47.5	47	47	47	46	45.5	45	45	45	45	4.	44.5	4.	44	44	44	44	44			44	44	m	43.5	m.
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hypothetical BCR/A	hypothetical prote	gag-abl-pol polypr	adenylate cyclase	hypothetical prote	kinase-related tra	protein-tyrosine k	hypothetical prote	nitrogenase cofact	trk system potassi	nitrogenase (EC 1.	transcription term	probable acylamino	ribonucleoside-dip	vp165 - rat	hypothetical prote
A24847	S61132	A26132	JS0029	B59106	A39962	TVHUA	H82231 -	S16047	AH0029	NIKBMA	S74003	D72636	E82223	I55441	F86211
4	N	N	_	(7)	C3	Н	N	N	N	Н	~	01	N	N	N
156	379	697	. 800	800	1123	1130	122	355	458	483	540	582	761	916	1061
34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.4
43.5	43.5	43.5	43.5	43.5	43.5	43.5	43	43	43	43	43	43	43	43	43
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1 A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat C;Species: Rattus norvegious (Norway rat) C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Aug-2004 C;Accession: A35007; A35700 B;Elshourbagy, N.A.; Near J.C.; Kmetz, P.J.; Sathe, G.M.; Southan, C.; Strickler, J.E.; J. Biol. Chem. 265, 1430-1435, 1990 A;Title: Rat ATP citrate-lyase. Molecular cloning and sequence analysis of a full-length A;Reference number: A35007; MUID:90110199; PMID:2295639 A;Reference number: A35007; MUID:90110199; PMID:2295639 A;Reference number: A35007 A;Readdues: 1-1100 cELES A;Residues: 1-1100 cELES A;Coss-references: UNIPROT:P16638; GB:J05210; NID:9949989; PIDN:AAA74463.1; PID:g203490 A;Title: Sequence of Sites on ATP-citrate lyase and phosphatase inhibitor 2 phosphorylat A;Reference number: A35700; MUID:91104719; PMID:2176822 A;Accession: A35700 A;Status: preliminary A;Molecule type: protein A;Residues: preliminary A;Molecule type: protein A;Residues: preliminary A;Molecule type: protein A;Residues: a18-459 <ram> C;Superfamily: ATP citrate synthase C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; phosphoprotein</ram>	rrickler, J.E.; a full-length l, PID:g203490 phosphorylate nn
 Query Match 41.6%; Score 52; DB 2; Length 1100; Best Local Similarity 40.0%; Pred. No. 8.3; Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0; Qy 1 IVAIIAGRIRMLGDQFNGELEASAK 25	
 RESULT 2 S2173 ATP citrate (pro-S)-lyase - human C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: S21173 R;Elshourbagy, N.A.; Near, J.C.; Kmetz, P.J.; Wells, T.N.C.; Groot, P.H.E.; Saxty, Bur. J. Biochem. 204, 491-499, 1992 A;Ritle: Cloning and expression of a human ATP-citrate lyase cDNA. A;Reference number: S21173 A;Accession: S21173 A;Accession: S21173 A;Residues: preliminary A;Molecule type: mRNA A;Residues: 1-1105 < ELS. A;Cross-references: UNIPROT:P53396; EMBL:X64330; NID:g28934; PIDN:CAA45614.1; PID:gC;Superfamily: ATP-citrate synthase	axty, B.A.;

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DB 2; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.0%; Score 47.5; DB 2; 45.5%; Pred. No. 4.7;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 LMSVRVKMKGDSTNGEQEAQKLN 140
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3 IMTIVKGRVRWIEGEQFIGRIE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain Orsay
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
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Matches 10; Conserv
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Best Local Similarity
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A; Residues: 1-146 < KAW>
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A; Status: preliminary
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H75111
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A; Residues: 1-319 sSWA>
A; Residues: 1-319 sSWA>
A; Cross-references: UNIPROT:Q07017; EMBL:L09654; NID:g153407; PIDN:AAA19695.1; PID:g1534
R:Swan, D.G.; Rodriguez, A.M.; Vilches, C.; Mendez, C.; Salas, J.A.
Mol. Gen. Canet. 242, 358-382, 1994
A; Title: Characterisation of a Streptomyces antibioticus gene encoding a type I polyketi
A; Riference number: 841729; MUID:94150470; PMID:8107683
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A,Residues: 1-579 <ROUJ-
A,Cross-references: UNIPROT:080953; EMBL:AC004697; NID:g3402671; PID:g3402693
A,Cross-references: Cultivar Columbia
A,Experimental source: Cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T02574

T02574

Mypothetical protein At2g39280 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein T16B24.8

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02574; D884815
B;Rounaley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, abumitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A;Reference number: Z14679
A;Accession: T02574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Status: nucleic acid sequence not shown
;Molecule type: DNA
;Residues: 1683-3358,3273-3303,'K',3305-3407,'T',3409-3462,'Y',3464-3516,'E',3518-3519
;Cross-references: BMBL:L09654
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Keywords: antibiotic biosynthesis; carrier protein

F9-462/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>

F970-851/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMII>

F970-851/Domain: short-chain alcohol dehydrogenase homology <SADI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1489-1560/Domain: acyl carrier protein homology <ACP1>
F;1708-2111/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0;
F;221-2502/Domain: [acyl-carrier-protein] synthase I homology <ACP2-2502/Domain: [acyl-carrier-protein] elmoyltransferase homology <AP 5:2689-3037/Domain: short-chain alcohol dehydrogenase homology <SAD2>
F;3143-3214/Domain: acyl carrier protein homology <ACP2>
F;3305-3500/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>
                                                 Gaps
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Score 52; DB 2; Length 1105; Pred. No. 8.3;
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30;
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Pred. No. 30;
8; Mismatches
                                               7; Mismatches
                                                                                                                                :|:: | :|:|| |:||| | |:|| | 924 LVSSLTSGLLTIGDRFGGALDAAAK 948
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                                                                                                 1 IVAIIAGRLRMLGDQFNGELEASAK 25
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  41.6%;
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ilarity 40.0%;
Conservative 8
                                                 Conservative
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  Query Match
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prophage pi3 protein 30 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Accession: C86600
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
A;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86800
A;Accession: C86800
A;Status: preliminary
A;Molecule type: DNA
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R;anonymous, Genoscope
Bubmitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
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A, Residues: 1-140 <STO>
A, Cross-references: UNIPROT: Q9CFR2; GB: AB005176; PID: g12724390; PIDN: AAK05501.1; GSPDB: GA
B, Experimental source: strain IL1403
C, Genetics:
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; FMID:10617197
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                                                                                                                                        A; Accession: D84815
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-579 <STO>
A; Cross-references: GB: AE002093; NID: G3402693; PIDN: AAC28996.1; GSPDB: GN00139
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PAB1905 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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A;Map position: 2
A;Introns: 219/3; 279/3; 317/3; 360/2; 382/3; 400/1; 428/1
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A;Gene: PAB1905
C;Superfamily: Escherichia coli hypothetical protein b3356
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Wixacaki, N.; Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

NAFes. 8, 205-213, 2001

NAFes. 8, 205-213, 2001

NAFes and A.; Tabata, S.

N. Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

NAFesternce number: AB1807; MUD:21595285; PMID:11759840

A,Reference number: AB1807; MUD:21595285; PMID:11759840

A,Status: preliminary

A,Molecule type: DNA

A,Residues: 1-36 «KUR»

A,Residues: 1-36 «KUR»

A,Fross-references: UNIPROT:Q8YM93; GB:BA000019; PIDN:BAB76742.1; PID:g17134181; GSPDB:GN

A,Experimental source: strain PCC 7120

C,Genetics: al15043

C,Superfamily: Escherichia coli spermidine/putrescine-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PH1469 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004 C;Accession: H71021 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine M.; Offuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an A;Reference number: A1000; MUID:98344137; PMID:9679194
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A; Residues: 1-132 <COL>
A; Cross-references: UNIPROT: O06133; GB: Z95554; GB: AL123456; NID: 93261771; PIDN: CAB08893.1
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A; Cross-references: UNIPROT:059138; GB:AP000006; NID:g3236133; PIDN:BAA30576.1; PID:g325;
A; Cross-references: UNIPROT:059138; GB:AP000006; NID:g3236133; PIDN:BAA30576.1; PID:g325;
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
A; Gene: PH1469
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A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230

A, Scateus: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70557
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A;Status: preliminary; nucleic acid sequence not shown; translation
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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Best Local Similarity
Matches 9; Conserv
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N.Alternate names: glycogen 6-glucanohydrolase
(Species Pectobacterium chrysanthemi
C;Dete: 01-Peb-2002 #sequence_revision 01-Peb-2002 #text_change 09-Jul-2004
C;Accession: JC7767 #sequence_revision 01-Peb-2002 #text_change 09-Jul-2004
C;Accession: JC7767 #sequence_revision 01-Peb-2002 #text_change 09-Jul-2004
S.Lim, W.J.; Park, S.R.; Cho, S.J.; Kim, M.K.; Ryu, S.K.; Hong, S.Y.; Seo, W.T.; Kim, H.
Biochem Biophys. Res. Commun. 287, 348-354, 2001
A;Title: Cloning and characterization of an intracellular isoamylase gene from Pectobact
A;Reference number: JC7767; PMID:11554733
A;Reference number: JC7767; PMID:11554733
A;Reference number: JC7767
A;Accession: JC7767
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polyamine-binding protein of polyamine ABC transporter all5043 [imported] - Nostoc polyamine-binding protein of polyamine ABC transporter all5043 [imported] - Nostoc Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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C;Superfamily: isoamylase type debranching enzyme
C;Keywords: glycosidase; hydrolase
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phosphatase (RapE) regulator phrE - Bacillus subtilis
C;Species: Bacillus subtilis
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C;Accession: B65677
E;Riust, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C;Accession: B65677
E;Riust, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C; Bron, S. D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
E;Ritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hulbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarvic, V.; Lee, B.; Rosen, J.; Liu, H.; Masuda, S.; Maueel,
A;Authors: Schleich, S.; Sonroeter, R.; Scoffone, P.; Schleich, T.M.; Portetelle,
A;Authors: Schleich, S.; Sonroeter, R.; Scoffone, P.; Sedone, J.; Schonsoter, N.; Taraka, T.; Terpstra, P.; Pognoni, A.; Tosato, V.; Vochiyama,
T.; Minters, P.; Wipat, A.; Tamaka, T.; Yoshidawa, H.; Danchin, A.; Tosato, V.; Yoshida, K.;
A;Authors: Sonkiawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Attle: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.
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Cypace: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cypace: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cypace: 31-Mar-2004
RyTettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Friekey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Frieker, Complete Sandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver, A.Title: Complete genome sequence of Neisseria meningidis serogroup B strain MC58.
A) Reference number: A81000; MUID:20175755; PMID:10710307
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A/Molecule type: DNA
A/Molecule type: DNA
A/Cross-references: UNIPROT:Q9K0T0; GB:AE002405; GB:AE002098; NID:g7225708; PIDN:AAF40927
A/Experimental source: serogroup B, strain MC58
A/Gene: NMB0493
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Pred. No. 3.8;
8; Mismatches 7;
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Pred. No. 2.8e+02;
5; Mismatches 3
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Best Local Similarity 39.4%; Pr
Matches 13; Conservative 5;
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Best Local Similarity 33.3%;
Matches 8; Conservative E
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A;Gene: phrE
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: YPO3545
C;Superfamily: probable transcription regulator ybbS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%; Score 45; DB 2; ilarity 45.0%; Pred. No. 95; Conservative 5; Mismatches
                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 2
Pred. No. 25;
6; Mismatches
                                                                                                                                                                 36.0%; Score 45; DB 58.8%; Pred. No. 10;
                                                                                                                                                                                                       Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAAGRIRVIGPEYSREAD 270
                                                                                                                                                                                                                                              5
A, Experimental source: strain H37Rv C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIAGRIRMIGDQFNGELE 21
                                                                                                                                                                                                                                                                                                                               7 GRLRMLGDQFNGELEAS 23
                                                                                                                                                                                                                                                                                                                                                                                                           GGLRMIHDLLHGELAAS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.45
Matches 8; Conservative
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
Molecule type: DNA
Residues: 1-297 <KUR>
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A; Residues: 1-996 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: AB0431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: AB0431
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C:Superfamily: pr
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                                                                                A; Gene: Rv1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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Search completed: November 10, 2004, 14:52:14 Job time : 7.37736 secs

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Aah56933

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Q9v0u4 Q89b89 Q071j0 Q071j0 Q9az68 Q9az68 Q9az68 Q9az68 Q9cfr2 Q9cfr2 Q9cia0 Q81gm8 Q7ndc6 Q8

lactococcus gallus gall gloeobacter

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TISSUB-Mammary gland;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MISSUB-Mammary gland;

MISSUB-Mammary gland;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027668; AAH27668.1; -.
NON TER 157 AA; 17078 MW; 92F95902186B5347 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Gm566 procein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 108; DB 2;
88.0%; Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                           157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8CHH7
Q9V0U4
Q89B89
Q77IJ0
Q9AYX5
Q9AZ68
Q9AZM9
                                                                                                                                                               Q9CIAO
O53060
Q8JGM8
Q7NDC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Query Match

Best Local Similarity

Best Local 22; Conservative
 and mouse cDNA sequences."
1223
1744
1744
1146
1221
1140
1140
1141
1193
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
. 44
44 . 44444444444
8888
                                                                                                                                                                                                                                                                                                                                                                             08K186;
                                                                                                                                                                                                                                                                                                                                                         Q8K186
                                                                                                                                                                                                                                                                                                                        RESULT 1
08K186
BUTTER SELECTION OF SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SE
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Q88394 homo sapien
Q91v92 mus musculu
P16638 rattus norv
D7336 homo sapien
Q70717 streptomyce
Q664967 brachydanio
C70640 pseudomonas
C752984 pseudomonas
Q75104 anopheles q
Q75104 anopheles q
Q75104 drosophila
080953 arabidopsis
Q88677 pseudomonas
Q71xc6 drosophila
Q71xc9 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shewanella
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aad34754 drosophil
Q7q0u7 anopheles g
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293rk2 haemophilus
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bordetella
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                                                                                                                                  (without alignments)
431.938 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                November 10, 2004, 13:38:57; Search time 34.634 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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Q7vz19
Q7wda8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ad52
Q8bix2
Q6pgm5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8ean7
Q99k05
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                                                                                                                                                                                                                                                                                                                                          1825181
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        1825181 segs, 575374646 residues
                                                                                                                                                                                                      125
1 IVAIIAGRLRMLGDQFNGELEASAKN 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08K186
098K37
099K05
08VDM8
07VZ19
07VZ19
07VZ19
08N9C4
08N9C4
08NYQ1
ACLY RAT
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OCLS GTRAT
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Q75UU6
Q07UUC6
Q080953
UVRC PSEPK
Q7KRA9
AAM70940
Q7KU85
AAD34754
Q7QUU7
Q7QUU3
Q9KUV3
Q9KUV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                                 - protein search, using sw model
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CAF32984
Q7PMH0
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Q8BIX2
Q6PGM5
                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum Match 100%
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seq length: 200000000
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Match Length
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579
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                                Copyright
                                                                                                                                                                                                                                                       BLOSUM62
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Sequence:
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Maximum DB
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Gaps

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Length 157;

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shavenko Y., Bouffard G.G., Shavenko Y., Bouffard G.G., Shaving M.C., Shevchenko Y., Bouffard G.G., Shaving M.C., Shavenko Y., Bouffard G.G., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C., Shaving M.C.,
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;

MEDINRE-238825; PubMed=1447932;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

Hopkins R.F., Jozdan H., Moore T., Max S.I., Mang J., Hsieh F.,

Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soarse M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Will M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Rack S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarartne P.H.,

Richards S., Worley K.C., Hals S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rack J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Misselbey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rack Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rack Blakesley R.W., Bulkerield Y.S.,

Rack Blakesley R.W., Bulkerield Y.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=mix FVB/N;
TISSUB=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 AA; 21693 MW; 68127314F9BB3404 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.6%; Score 52; DB 2;
40.0%; Pred. No. 12;
rative 7; Mismatches 8
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acly protein (Fragment). Name=Acly;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE_22297686; PubMed=12368813; DOI=10.1038/nbt749;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadra R., Ward N.L., Methe B.A.,
Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
Haft D.H., Kolonay J. F., Madupu R., Peterson J.D., Umayam L.A.,
White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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TISSUB=Mammary tumor. WAP-TGF alpha model. 7 months old;
MEDLINE=22386257, PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
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GO, GO.005489; F.electron transporter activity; IBA.
GO; GO.0005566; F.iron ion binding; IEA.
GO; GO:0006118; P.electron transport; IEA.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR004453; FeSclus binding.
InterPro; IPR009051; Helical_ferredxn.
                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Iron-sulfur cluster-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99K05;
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Acly protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 42.4%; Score 53; DB 2; Similarity 57.9%; Pred. No. 16; 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 AA
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TIGRFAMs; TIGR00276; FeSclus_binding; 1.
PROSITE; PS00198; 4FE45_FERREDOXIN; 1.
                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
EMBL, AE015819; AAN56837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Best Local Similarity
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01-MAR-2004 (
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                                                                                                                                                          Q8EAN7
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Q99K05
                                                                          RESULT 2
                                                                                                                     Q8EAN7
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Score 52; DB 2; Length 682; Pred. No. 40; 6; Mismatches 5; Indels

70475 MW; D8F2FC7842B168B8 CRC64;

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/ Match 41.6%; Score 52; Local Similarity 48.0%; Pred. No. one 12; Conservative 6; Mismatch
                                                                682 AA;
                   Complete proteome. SEQUENCE 682 AA;
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01-OCT-2003
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Q8N9C4;
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Matches
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QBN9C4
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SEQUENCE FROM N.A.

CSTRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22807954; PubMed=12910271; DOI=10.1038/ng1227;
A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., A chriman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Corlingworth T., Collins M., Cronin A., Davis P., Doggett J., Chillingworth T., Gollins M., Cronin A., Davis P., Doggett J., Relwell T., Gobbe A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch B., Ruter S., Sanders M., Saunders D., Seger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J., Romparative analysis of the genome sequences of Bordetella pertussis, M. Conton D., Price C., M. Comparative analysis of the genome sequences of Bordetella pertussis, M. Conton D., Price C., M. Comparative analysis of the genome sequences of Bordetella pertussis, M. Conton D., Price C., M. Conton D., Price C., M. Comparative analysis of the genome sequences of Bordetella pertussis, M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M. Conton D., Price C., M.
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.6%; Score 52; DB 2; Length 592;
40.0%; Pred. No. 35;
ive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC021502, AAH21502.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:103251; Acly.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0004108; F:citrate (Si)-synthase activity; IEA.
GO; GO:0004108; P:citrate, IEA.
GO; GO:0006152; P:metabolism; IEA.
GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
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Last annotation update)
                                                                                                                                                                                                  Proc. Natl. Acad, Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS01216; SUCCINYL COA LIG 1; 1.
PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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Interpro; IPR003781; CoA binding.
Interpro; IPR005811; CoA ligase.
Interpro; IPR005810; CoA ligalpha.
Pfam; PF02629; CoA binding; 1.
Pfam; PF00549; Ligase_CoA; 1.
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TIGREAMS; TIGR00733; OPT fam; 1.
TIGRFAMS; TIGR00728; OPT_sfam; 1.
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01-0CT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                     cDNA sequences.
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SEQUENCE
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O7VZI
D7 O2VZI
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SEQUENCE FROM N.A.

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STRAIN=RBSD / ATCC BAA-588;

MEDLINE=22827954, PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cedeno-Tarraga A. H., Temple L., James K.D., Harris B., Quail M.A.,

A Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Comparative praparetussis and Bordetella bronchiseptica.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71698 MW; 71F130E7BD611A88 CRC64;
                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ37765.
                                                                                                                                                                                                                       693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                    :|:: ||:|||:||| |:|||
191 LVSLATGGLRVLGDSFSWWGQLGAS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004814; Oligopep_transpt.
InterPro; IPR004813; Tetrpept_transpt.
Pfam; PF03169; OPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVAIIAGRLRMLGDQFN--GELEAS 23
1 IVALIAGRIRMIGDOFN--GELEAS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGREAMS; TIGRO0733; OPT fam; 1.
IGREAMS; TIGRO0728; OPT_sfam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.68;
48.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX640448; CAE35643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                              Putative membrane protein.
OrderedLocusNames=BB3670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=518;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                  [2]
SEQUENCE FROM N.A.
               FROM N.A
                                             MEDLINE=96305350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACLY MOUSE
Q91V92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ACLY MOUSE
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154F
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                                      RA Pubmed=14702039;

RA Pakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sadito K., Xawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Jakahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Takahashi M., Matanabe M., Hiraoka M., Hotuta T., Kusano J.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka M., Hotuta T., Kusano J.,

RA Todiya S., Komai F., Hara R., Takauchi K., Arita M., Imose N.,

RA Musashino K., Yuuki H., Oshima A., Saaski M., Aotsuka S.,

RA Moriya S., Komai F., Hara R., Takauchi K., Arita M., Imose N.,

RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,

Noshikawa Y., Matanabe K., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Yomazaki M., Watanabe K., Xuuki H., Tahigami S., Terashima Y., Suzuki O.,

RA Yamazaki M., Watanabe K., Kuusaya A., Takemoto M., Kawakami B.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Tekamotu Y., Okamoto S.,

RA Yamazaki M., Watanabe K., Xuusaya A., Takemoto M., Kawakami B.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Tekamotu M., Sasaki M.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Takayawa K.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Takayawa K.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Takayawa K.,

Rujimori Y., Makajima Y., Mizuno T., Morinaga M., Sasaki M.,

Rawabata A., Hikiji T., Kobatek N., Inagaki H., Ikama Y., Okamoto S.,

Rawabata A., Hikiji T., Kobatek N., Inagaki H., Ikama Y.,

Rawabata A., Hikiji T., Kobatek N., Inagaki H., Ikama Y.,

Rayabami R., Nadasa T., Noguchi S., Itoh T., Shigeta K., Senba T.,

Rayabimura K., Nadasa T., Matanabe T., Shirai Y., Takahashi Y., Nakagawa K.,

Rayabima K., Yada T., Nakamura Y., Ohara O., Isoga T., Nakasuhita R.,

Rujima M., Watanaba H., Nakai Y., Matanio M., Kawaki H.,

Rayashi M., Watanaba H., Nakai W., Wasuho Y., Ya
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 0003824; F: catalytic activity; IEA.
GO; GO: 0004108; F: citrate (Si)-synthase activity; IEA.
GO; GO: 0006152; P: metabolism; IEA.
GO; GO: 0006059; P: tricarboxylic acid cycle; IEA.
InterPro; IPR002020; Citrate synth.
InterPro; IPR00381; Coa_binding.
InterPro; IPR00581; Coa_binding.
InterPro; IPR00581; Coa_binding.
InterPro; IPR00581; Coa_binding.
InterPro; IPR05810; Coa_binding.
InterPro; IPR05810; Coa_binding.
InterPro; IPR05810; Coa_binding.
InterPro; IPR0589; Ligase Coa; I.
FEam; PF00549; Ligase Coa; I.
FEam; PF00549; SCOASYNTHASE.
PROSITE; PS01216; SUCCINVL. Coa_LiG_2; I.
SROUENCE 701 AA; 76445 WW; 4BEFC567E3D57852 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
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520 LVSSLTSGLLTIGDRFGGALDAAAK 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Genet. 36:40-45(2004).
EMBL; AK095084; BAC04484.1; -.
HSSP; P07459; lJKJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-citrate lyase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 20, TrEMBLrel. 20, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                   TISSUE=Hippocampus;
PubMed=14702039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=ACL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Moon Y.A., Kim K.S., Park S.W., Kim Y.S., arcloning and identification of exon-intron organization of the rat ATP-citrate lyase gene."; Biochim. Biophys. Acta 1307:280-284(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L47319; AAL3416.1; ...

REMBL; L47319; AAL34316.1; ...

REMBL; L47319; AAL34316.1; ...

REMBL; L47310; AAL34316.1; JOINED.

REMBL; L47310; AAL34316.1; JOINED.

REMBL; L47310; AAL34316.1; JOINED.

REMBL; L47310; AAL34316.1; JOINED.

REMBL; L47310; AAL34316.1; JOINED.

REMBL; L47314; AAL34316.1; JOINED.

REMBL; L47314; AAL34316.1; JOINED.

REMBL; L47314; AAL34316.1; JOINED.

REMBL; L47314; AAL34316.1; JOINED.

REMBL; L47314; AAL34316.1; JOINED.

REMBL; L47313; AAL34316.1; JOINED.

REMBL; L47313; AAL34316.1; JOINED.

REMBL; L47313; AAL34316.1; JOINED.

REMBL; L47313; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; AAL34316.1; JOINED.

REMBL; L47301; JOINED.

REMBL; L47301; JOINED.

REMBL; L47301; JOINED.

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REMBL; L47301; JOINED.

REMBL; L47301; JOINED.

REMBL; L47301; JOINED.

REMBL; L47301; JOINED.

REMBL; L
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SEQUENCE 851 AA; 92479 MW; 0717514686408CA0 CRC64;
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PROSITE; PS01399; SUCCINYL_COA_LIG_2; 1.
PROSITE; PS01217; SUCCINYL_COA_LIG_3; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.6%; Score 52; DB 2;
40.0%; Pred. No. 50;
iive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
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670 LVSSLTSGLLTIGDRFGGALDAAAK 694
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                                                                                                                                                                                                                                                                                        TISSUE=Liver;
MEDLINE=90110199; PubMed=2295639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01798; SCOASYNTHAS
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Pfam; PF00549; Ligase CoA; 1
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STRAIN=CSTEL/6; TISSUE=Brain;

MEDLINE=228825; PubMed=12477922; DOI=10.1073/pnas.242603899;

MEDLINE=228825; PubMed=12477922; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Maxx. El., Wang J., Habt N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaug G.G.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaug G.G.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

Butkerfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are extrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.cib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: ATP citrate-lyaes is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. Has a central role in de novo lipid synthesis. In nervous tissue it may be involved in the biosynthesis of acetylcholine (By similarity).
-!- CATALYTIC ACTIVITY: ADP + phosphate + acetyl-CoA + oxaloacetate =
                                                                                                                                                                                                                                                                                                                                                 STRAIN=IES, and ISS, MEDINE=21363810; PubMed=11471062; Xu Y., Yang F., Canniff J., Enringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J., Besson M., Gornon I., Bennett B., Johnson T.E., Sikela J.M.; "High-throughput sequence identification of gene coding variants within alcohol-related Offis:";
                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
05-JUL-2004 (Rel. 44, Last annotation update)
ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
(Citrate cleavage enzyme).
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: In the N-terminal section, belongs to the succinate/malate CoA ligase beta subunit family.
-!- SIMILARITY: In the C-terminal section, belongs to the succinate/malate CoA ligase alpha subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002020; Citrate synth. InterPro; IPR003781; CoA binding. InterPro; IPR05811; CoA ligase. InterPro; IPR05810; CoA ligase. InterPro; IPR05809; CoA ligate. PF02629; CoA binding; IPR05899; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR0589; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; CoA binding; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05899; IPR05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm. Genome 12:657-663(2001).
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                                                                                                                                                                                                                                                                                                                                                                                           ö
Pfam; PF00549; Ligase CoA; 1.
PROSITE; PS01216; SUCCINYL COA LIG 1; 1.
PROSITE; PS00399; SUCCINYL COA LIG 2; 1.
PROSITE; PS01227; SUCCINYL COA LIG 3; 1.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
ATP-binding; Lipid synthesis; Magnesium; Phosphorylation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ATP cittate-lyse is the primary enzyme responsible for FUNCTION: ATP cittate-lyse is the primary enzyme responsible for central role in de novo lipid synthesis. In nervous tissue it may be involved in the biosynthesis of acetylcholine. ATALYTIC ACTIVITY: ADP + phosphate + acetyl-CoA + oxaloacetate = ATP + citrate + CoA.

ENZYME REGULATION: Major regulation of ATP citrate-lyase activity altering the amount of enzyme. SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90110199; PubMed=2295639;
Elshourbagy N.A., Near J.C., Kmetz P.J., Sathe G.M., Southan C.,
Strickler J.E., Gross M., Young J.F., Wells T.N.C., Groot P.H.E.;
"Rat ATP citrate-lyase. Molecular cloning and sequence analysis of a
full-length cDNA and mRNA abundance as a function of diet, organ, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - SUBCEDIVILAR LOCATION: Cytoplasmic.
- SUBCEDIVILAR LOCATION: Cytoplasmic.
- PTM: Phosphorylated on two regulatory serines. The ability to phosphorylate at either one of the regulatory sites depends of phosphorylation state of the other regulatory site.
- PTM: The N-terminus is blocked.
- SIMILARITY: In the N-terminal section, belongs to the succinate/malate CoA ligase beta subunit family.
- SIMILARITY: In the C-terminal section, belongs to the succinate/malate CoA ligase alpha subunit family.
                                                                                                                                                                                            COA-binding (Potential).
Phosphoserine (by PKA) (By similari
Tale-phosphohistidine intermediate
similarity).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-CTT-2004 (Rel. 45, Last annotation update)
ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                               Magnesium (By similarity).
W; 660293D027D797DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1100 AA.
                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                 Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 LVSSLTSGLLTIGDRFGGALDAAAK 934
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                                                                                                                                                                                                                                                                                                      1091 AA; 119727 MW;
                                                                                                                                                                                                                                                                                                                                                 41.68;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Citrate cleavage enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Acly;
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P16638;
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                                                  R PIR; A35027; A35037.

R HSSP; P07459; ISCU.

R RGD; 2018; Acly.

R InterPro; IPR003781; CoA binding.

R InterPro; IPR003781; CoA binding.

R InterPro; IPR005811; CoA lig alpha.

R InterPro; IPR005809; CoA lig alpha.

R Pfam; PF02629; CoA binding; I.

R Pfam; PF02629; CoA binding; I.

R PROSITE; PS01216; SUCCINVL COA LIG 1; 1.

R PROSITE; PS01219; SUCCINVL COA LIG 1; 1.

R PROSITE; PS01219; SUCCINVL COA LIG 3; 1.

R ATP-binding; Direct protein sequencing; Lipid synthesis; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Variant.cDNA sequences of human ATP.citrate lyase: cloning, expression, and purification from baculovirus-infected insect cells."; Protein Expr. Purif. 9:133-141(1997).
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MEDLINE-2238557; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2238257; Pringold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elshourbagy N.A., Near J.C., Kmetz P.J., Wells T.N.C., Groot P.H., Saxry B.A., Hughes S.A., Franklin M., Gloger I.S.; "Cloning and expression of a human ATP-citrate lyase cDNA."; Eur. J. Biochem. 204:191-499(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97177247; PubMed=9116495;
Lord K.A., Wang X.M., Simmons S.J., Bruckner R.C., Loscig J.,
O'Connor B., Bentley R., Smallwood A., Chadwick C.C., Stevis P.E.,
Cicoarelli R.B.;
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                                                                                                                                                                                                                                                                                                                                                                       ATP (By similarity).

CoA-binding (Potential).

Phosphoserine (by PKA).

Tele-phospholistidine intermediate.
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P53396; Q13037; Q9BRL0;
O1-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
(Citrate cleavage enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 1; Length 1100;
Pred. No. 65;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnesium (By similarity). W; 2C6BE4BC1F53BDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                      ATP (By similarity).
or send an email to license@isb-sib.ch).
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454 454 Phos
759 759 Tele
717 717 Magn
1100 AA; 120635 MW;
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                                                                                                                                                                                                                                                                                                                                 Phosphorylation, Transferase.
NP_BIND 700 720 F
NP_BIND 751 777 F
DOMAIN 778 788 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.68;
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                                 EMBL; J05210; AAA74463.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
ACT_SITE
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SEQUENCE
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ACLY_HOVAN
DO ACLY_HOVAN
DO PS3396,
DT 08-701-701
DE ATP-COTT
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Hopkins P. P. Jodesh S. P. Beneow K. H. Scheeker C. P. Bara N. K.,

Hopkins P. P. Jodesh H. Moore T. Max S. I., Ward J. Histoh F. P.

Bitchembo L. Walladian H. Moore T. Max S. I., Ward J. Histoh F. P.

Barasas S. L. Jodesh H. M. Scares M. B., Bonaldo M. F., Casavant T. L., Scheeker T. E.,

Barasas S. J. Modellano N. M. Benaldo M. F., Casavant T. L. Scheeker T. E.,

Barasas S. J. Modellano N. M. Peres C. J. Make J. M. M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M. John M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R InterPro; IPR001227; Ac_Transferase.
R InterPro; IPR001227; Ac_Transferase.
R InterPro; IPR001227; Ac_Transferase.
R InterPro; IPR001024; Fatharyl synth.
R InterPro; IPR00103; Pp bind.
R InterPro; IPR001031; Thioesterase.
R Pfam; PF00109; ketoacyl-synt; 2.
R Pfam; PF00109; ketoacyl-synt; 2.
R Pfam; PF00109; Thioesterase.
R Pfam; PF00109; Thioesterase; 1.
R Pfam; PF00109; PF00109; C; 2.
R Pfam; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; PF00109; 
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-!- COFACTOR: Contains 2 covalently bound phosphopantetheines.
-!- SIMILARITY: Contains 2 acyl carrier domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1890;
                                                                                                                                                                                                                                                            Score 52; DB 1; Length 1101;
Pred. No. 65;
E -> V (in Ref. 1).
LGHRP -> WAPA (in Ref. 1).
SGS -> QRE (in Ref. 1).
SES -> YESNVDEV (in Ref. 1).
RPGS -> PQAA (in Ref. 1).
C -> S (in Ref. 1).
V -> A (in Ref. 1).
AGXD -> TAVE (in Ref. 1).
AGXD -> TAVE (in Ref. 1).
AGXD -> TAVE (in Ref. 1).
MW; 5CC770685DCBC23B CRC64;
                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Oleandomycin polyketide synthase, modules 5 and 6.
Name=orfB;
                                                                                                                                                                                                                                                                                     Pred. No. 65; 7; Mismatches
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L09654; AAA19695.1; -.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                           120825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
     444
4453
4459
656
872
919
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HSSP; Q03133; 1MO2.
                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
     245
419
442
457
653
728
872
1101
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OLS6_STRAT
ID OLS6_STRAT
AC Q07017;
CONFLICT
CONFLICT
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SEQUENCE
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Straubherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B. S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

A papteron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonaldo M.F., Carannor P.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; (uanio rerio).
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes; NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                  Phosphopantetheine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                Phosphopantetheine (By similarity)
W; 41AE78AAAEB61F86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 1; Length 3519;
Pred. No. 2.1e+02;
3; Mismatches 7; Indels
Beta-ketoacyl synthase 1.
Acylransferase (ATN 1 .
Beta-ketoacyl synthase 1.
Acyl carrier (ACP) 1.
Beta-ketoacyl synthase 2.
Acylransferase (ATN 2 .
Beta-ketoacyl reductase 2.
Acyl carrier (ACP) 2.
Thioesterase.
Beta-ketoacyl synthase.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC076484; AAH76484.1; -.
Hypothetical protein.
SEQUENCE 1092 AA, 119709 WW, 5E8003F5327B30B3 CRC64;
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                                                                                                                                                                                                                                                                                                                          Beta-ketoacyl synthase.
Acyl-ester intermediate.
                                                                                                                                                                                                                                                 Acyl-ester intermediate.
NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1092 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Whole;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                       368561 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0
Matches 10; Conservative
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     501
890
1382
1561
2156
2541
3038
3215
3519
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TISSUE=Whole;
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                                                                                                                                                                                                                                                                                                                          1859
2311
2859
3178
3519
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ACT_SITE
NP_BIND
BINDING
SEQUENCE
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ACT_SITE
NP_BIND
BINDING
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DOMAIN
DOMAIN
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Q6DG67
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Bertani I., Venturi V.;
"Regulation of the N-acyl homoserine lactone dependent quorum sensing system in rhizosphere Pseudomonas putida WCS358 and cross-talk with the stationary phase RpoS sigma factor and the global regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                Gaps
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Pseudomonadaceae; Pseudomonas.
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Pseudomonadaceae; Pseudomonas.
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SUBMILLED (WAR-2004) LO THE EMBL/GenBank/DDBJ databases.

SUBMILLED (MAR-2004) LO THE EMBL/GenBank/DDBJ databases.

REMBL; AJG29219, CAR32884.1; -..

RINTERPRO; IPR001943; UVRB/C.

RINTERPRO; IPR003035; UVRB/C.

R Pfam; PF02151; UVR; 1..

Pfam; PF02151; UVR; 1..

R SMART; SM00465; GIYC; 1..

R PROSITE; PS50154; UVR; 1..

R PROSITE; PS50164; UVR; 1..

R PROSITE; PS50164; UVR; 1..

R PROSITE; PS50164; UVR; 1..
40.8%; Score 51; DB 2; Length 1092; 36.0%; Pred. No. 92; ive 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%; Score 49; DB 2; Length 248; ilarity 39.1%; Pred. No. 43; Conservative 6; Mismatches 8; Indels
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJG29219; CAF32884.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 248 27994 MW; 76119C2F2367F398 CRC64;
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10-MAR-2004 (TrEMBLrel. 27, Last sequence update)
10-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
UVC protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AA.
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                                                  Best Local Similarity 36.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE
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         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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SQ SEQUENCE 248 AA; 27994 MW; 76119C2F2367F338 CRC64;

Query Match
39.2%; Score 49; DB 2; Length 248;

Best Local Similarity 39.1%; Pred. No. 43;

Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps

Qy 2 VAIIAGRLRMLGDQFNGELEASA 24

Db 195 WMFLEGRSQQLGNELNAEMERAA 217

Search completed: November 10, 2004, 14:49:58

Job time: 36.634 secs
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November 10, 2004, 13:44:14; Search time 10.6151 Seconds (without alignments) 181.178 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

US-10-092-750-45 143 1 LALAYYSSRQYASALKHIĄEIIERGIRQH 29

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

478139 seqs, 66318000 residues Searched:

478139 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodate/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodate/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodate/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodate/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodate/1/iaa/PcTUS\_COMB.pep:\*
6: /cgn2\_6/ptodate/1/iaa/PcTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		p				
Result		Query				
No.	Score	Match	Length	60	QI	Description
п	51		~ ~	7	-08-248-466B-	equence 8, Appl
7	51	35.7	301	4	-09-489-039A-111	equence 11121,
٣		ω.	87	m	-134-001C-30	3005
4	œ,	۳.	a	4	-09-710-279-311	equence 3114,
w	48.5	33.9	CV	4	-09-710-279-31	equence 3130,
9	œ,	ω.	N	ო	-09-134-001C-537	e 5379,
7	8	ω.	m	ო	-134-001C-29	equence 2907,
œ	æ,	33.9	m	m	-09-134-001C-290	53
σ	48	ε,	9	-	-951-715A-2	equence 25
10	48	ë,	9	N	-08-459-448A-2	25
11	48	ω.	9	m	-08-459-595A-2	25
12	48	ω.	ø	m	-08-459-504B-2	25
13	48	33.6	9	m	08-459-444-2	ò
14		ω,	9	m	-09-547-422-2	ò
15	48	۳.	ø	4	-09-988-4	25
16	48	ъ.	473	4	-09-538-092-	133
17	47	•	757	4	US-09-494-297A-2	2,
18	46.5	ά.	g	4	-46	9.49
19	46	32.2	203	4	-09-270-76	3495
20		ď	0	4	-09-270-767-5016	equence 50
21	46	ć,	α	4	-09-602-787A-2	equence 26
22	46	ď	σ	ო	-09-362-899-	equence 3, App
23			m	4	-09-270-767-5690	equence 56909,
24	45	ä	~	4	-09-270-767-416	e 41
25	45	•	$^{\circ}$	4	-09-583-110-42	e 4292,
56	44.5	ä	m	ო	-09-134-001C-45	e 4549,
27	4.	31.1	~	4	-352-524	5243,

35.7%; Score 51; DB 1; Length 224;

Query Match

Sequence 17867, A	Sequence 2, Appli	Seguence 7721, Ap	Sequence 8880, Ap	Sequence 1, Appli	Sequence 3, Appli	Sequence 21535, A	Sequence 334, App	Sequence 898, App	Sequence 1134, Ap	Sequence 7058, Ap	Sequence 40, Appl	Sequence 40, Appl	Sequence 36552, A	Seguence 51769, A	Sequence 41, Appl	Sequence 3999, Ap	Sequence 164, App
US-09-248-796A-17867	US-09-029-047C-2	US-09-621-976-7721	US-09-489-039A-8880	US-08-764-343-1	US-08-989-925-3	US-09-252-991A-21535	US-09-538-092-334	US-09-710-279-898	US-09-710-279-1134	US-09-328-352-7058	US-08-258-287B-40	US-08-368-704C-40	US-09-270-767-36552	US-09-270-767-51769	US-08-602-359A-41	US-09-134-000C-3999	US-08-679-493A-164
4	マ	4	4	٦	N	4	4	4	4	4	m	m	4,	4	N	4	m
474	2644	86	315	437	437	196	1025	224	224	243	171	171	240	240	311	355	495
31.1	31.1	30.8	30.8	30.8	30.8	30.8	30.8	30.4	30.4	30.4	30.1	30.1	30.1	30.1	30.1	30.1	30.1
44.5	44.5	44	44	44	44	44	44	43.5	43.5	43.5	43	43	43	43	43	43	43
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 5379, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
DUCECTE-Stamm et al
TITLE OF INVENTION:
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Fatent No. 6703492

GENERAL INPORMATION

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ48002

FULLE REFERENCE: 19048002

CURRENT APPLICATION NUMBER: 05/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver: 2.1

LENGTH: 224
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILTE SEPRENCE: PU3-480US
CURRENT PELICATION NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: US/09/11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
SOFTWARE: PATENTIN OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: amino acid sequence US-09-710-279-3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: amino acid sequence
US-09-710-279-3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 224;
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Best Local Similarity 40.0%; Pred. No. 14;
Matches 12; Conservative 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LALAYYSSRQYASALKHIAEII-ERGIRQH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 VAVGYY--LRYALSYRDISEILRERGVNVH 43
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Pred. No. 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 12; Conserva
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US-09-134-001C-5379
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US-09-710-279-3130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
                                                                                                                                                                                                                                                                                                                                                                    Sequence 11121, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11121
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                                                    Gaps
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                                                7; Indels
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        Similarity 33.3%; Pred. No. 5.8; 9; Conservative 11; Mismatches
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Pred. No. 8.1;
9; Mismatches
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                                                                                                                                                                          |:| |:| |: | : : : | : : : | | : LSYVSSKQEAYSKRNVAKYLKKAIEQY 212
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                                                                                                                         3 LAYYSSRQYASALKHIAEIIERGIRQH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LALAYYSSRQYASALKHIAEIIERGIR 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3114, Application US/09710279; Patent No. 6703492; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-3005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Klebsiella pneumoniae US-09-489-039A-11121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .c..
1 Similarity 40.7%;
11; Conservative
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Best Local Similarity
Matches 12; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-489-039A-11121
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US-09-134-001C-3005
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US-09-710-279-3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Dunder, Erik M.
APPLICANT: Bace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INBECTICIDAL ACTIVITY IN MAIZE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "protein sequence for soybean CDPK as shown in Figure 34."
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
FRIOR APPLICATION: 800
FRIOR APPLICATION: 800
FRICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPINII, W. MALFAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 3-943
REGISTRATION NUMBER: 3-18805/A/CGC 1577/CIP
TELEPHONE: (19.9)541-8615
TELEPHONE: (19.9)541-8615
TELEFAX: (9.19)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
                                                     ADDRESSEE: CIER-GEIGY Corporation STREET: 7 Skyline Drive CITY: Hawthorne CITY: Hawthorne COUNTRY: USA ZIP: 10532
                                                                                                                                                              US-07-951-715A-25
; Sequence 25, Application US/07951715A
; Patent No. 5625136
                                                                                                                                                                                                                                             Tr. Koziei, Michael G.
Tr. Desai, Nalini M.
Tr. Iewis, Kelly S.
Tr. Kramer, Vance C.
Tr. Warren, Gregory W.
F. Evola, Stephen V.
F. Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Zrik M.
Pace, Carry
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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) OTHER INFORMATION:

) OTHER INFORMATION:

US-07-951-715A-25
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Best Local Similarity
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US-09-134-001C-2908

Sequence 2908, Application US/09134001C

Sequence 2908, Application US/09134001C

RELEASE INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/054,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2908

LENGTH: 230
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US-09-134-001C-2907

US-09-134-001C-2907

Sequence 2907, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WUGLER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-11-08

PRIOR PLICATION NUMBER: US 60/064,964

PRIOR PLICATION NUMBER: US 60/055,779

PRIOR PLING DATE: 1997-11-08

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2907

LENGTH: 230
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                                                                                                                                                                                            DB 3; Length 229;
                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                          8; Mismatches
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21 VAVGYY--LRYALSYRDISEILRERGVNVH 48
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1 Similarity 40.0%; Pred. No. 14
12; Conservative 8; Mismatche
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2908
                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5379
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5379
LENGTH: 229
                                                                                                                                                                                                              Best Local Similarity
Matches 12; Conserv
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Fri Nov 12 14:55:28 2004

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Gaps
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APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
, OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-448A-25
                                                                    Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESTORDENCE AUDRESS:
CORRESTORDENCE AUDRESS:
STREET: Patent & Trademark Dept., 520 White Plains STREET: Patent & Trademark Dept., 520 White Plains STREET: Patent & Trademark Dept., 520 White Plains CITY: Tarrytewn
STREET: New York
COUNTY: USA
ZIE: 10591-9005
COMPUTER: READABLE FORM:
MEDIUM TYPE: Flopsy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-UNN-1995
CLASSIFICATION: BOWTA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40403
REGISTRATION NUMBER: CGC 1577/CIP/DIV3
                                                                                                                Indels
                                                               Score 48; DB 2;
Pred. No. 38;
4; Mismatches
                                                                                                                                                                                                                                                                          RESULT 11
US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                         :|| || | :| ||:|
108 HYSERQAARLIKTIVEVVE 126
                                                                                                                                                              5 YYSSRQYASALKHIAEIIE 23
                                                                                                                                                                                                                                                                                                                                                                                        Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kramer, Vance C.
Warren, Gregory W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
                                                                 Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (919)541-858
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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    Gaps
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: 10591-9005

ZIP: 10591-9005

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION NUMBER: CGC 1577/CIP/DIV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
    .
9
  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX. (919)541-856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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us-10-092-750-45.rai

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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: No. 6111014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 2.5-EP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/ACENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 8-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-6587
TELEPHONE: (919) 541-6587
TELEPHONE: (919) 541-6687
TELEPHONE: (919) 541-6687
TELEPHONE: (919) 541-6687
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TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTER TO USA
ZIP: 27709
ZIP: 27709
COMPUTER READELE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNHER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                              /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%; Score 48; DB
47.4%; Pred. No. 38;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-459-444-25
US-08-459-444-25
Sequence 0, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 HYSERQAARLIKTIVEVVE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YYSSRQYASALKHIAEIIE 23
                            LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.44
Matches 9; Conservative
   SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                            FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: 67
US-08-459-5048-25
                                                                                                                                 linear
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APPLICANT: Warren, Gregory W.
APPLICANT: Warren, Gregory W.
APPLICANT: Brola, Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowman, Clindy G.
APPLICANT: Dawson, John L.
APPLICANT: Bowson, John L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: PROC. Gary M.
APPLICANT: PROC. Gary M.
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APPLICANT: PROC. GARY M.
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                                                                                                                                     /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                               Query Match 33.6%; Score 48; DB 3; Length 463; Best Local Similarity 47.4%; Pred. No. 38; Matches 9; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 27709
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Neigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GCC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: No. 6075185artis Corporation
SSEE: No. 6075185artis Corporation
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-UUN-1995
APPLICATION UNDRABE: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/08459504B Patent No. 6075185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YYSSRQYASALKHIAEIIE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desai, Nalini M.
Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SECUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075186
STREET: 3054 Cornwalli
CITY: Research Triangli
STATE: NC
HYPOTHETICAL: NO
FRATURE:
NAMMYKEY: Protein
LOCATION: 1..463
OTHER INFORMATION:
OTHER INFORMATION:
US-08-459-595A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-459-504B-25
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Gaps

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APPLICANT: Koziel, Michael G.

APPLICANT: Koziel, Malini M.
Lewis, Kelly S.
Kramer, Vance C.
Marren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
INTLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA
ZIP: 27709
COUNTYER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIFICATION NUMBER: US/09/984,462
FILING DATE: 11-APR-200
APPLICATION NUMBER: US 09/547,422
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/772,027
FILING DATE: UT THANDALLION:
NUMBER: US 07/772,027
                                                                                                                                                                                                                            DB 3; Length 463;
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSE:
SADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                            Score 48; DB 3
Pred. No. 38;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: S-188051 TELECOMMUNICATION INFORMATION:
                                                                                                                                     LOCATION: 1..463
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-988-462-25; Sequence 25, Application US/09988462
Patent No. 6720488
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 463 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      5 YYSSRQYASALKHIAEIIE 23
  STRANDEDNESS: single
                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS
                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
                                                                                                               NAME/KEY:
                                                                                                                                                                                 US-09-547-422-25
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSER:
ADDRESSER:
O'STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELETAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "protein sequence for soybean CDPK as shown in Figure 34."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: READABLE FORM:
MEDIUM TYPE: Flopey disk
COMPUTER: END FC compatible
COMPUTER: END FC compatible
COMPUTER: END FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-APPL-2000
FILING DATE: 11-APPL-2000
PRIOR APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SPF-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 04-OCT-1991
ATTORING AGENT INFORMATION:
NAME: Meigs, U Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    Length 463;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                    Score 48; DB 3;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                     LOCATION: 1.463

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koziel, Michael G.
Desal, Nalini M.
Lewis, Karly S.
Kramer, Vance C.
Warren, Gregory W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 0, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       108 HÝSERQAARLIKTÍVEVVE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                            5 YYSSRQYASALKHIAEIIE 23
                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FEATURE:
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative 4
                                                                                                                                  NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 94
TYPE: amino acid
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-547-422-25
                                                                                                                                                                                                                                                                                                                                                                                     d
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STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRATURE:

LOCATION: 1..463

OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-988-462-25
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Search completed: November 10, 2004, 14:55:34 Job time: 11.6651 secs

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5 YYSSROYASALKHIAEIIE 23

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0; Gaps

Query Match
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 4; Mismatches 6; Indels

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November 11, 2004, 01:28:30; Search time 33:5415 Seconds (without alignments) 305:399 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/SPCT_MBW_PUB_pep:*

3: \cgn2_6/ptodata/1/pubpaa/SPCT_MBW_PUB_pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_MBW_PUB_pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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9: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USIOR_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USIOR_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USIOR_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USIOR_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

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19: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USIOR_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LALAYYSSRQYASALKHIAEIIERGIRQH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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143
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	•	:	pl	Ap	Ap	ď	p]	App,	`	ď	~	ď	∢	4	Ą
			5, A	3203,	2099,	5, A	74, Appl	106, 7	276504,	32647, A	281833	53395,	64162,	72211,	60515,
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	Description		Sequence 45, App.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		1 1 1 1 1		m	0				504	47	833	95	62	11	515
		-	0-45	9-320	9-209	0-55	2-74	3-106	5-276	1-326	5-281	4-533	4-641	4-722	2A-60
		!	92-75	94-74	94-74	86-72	10-17	59-49	25-11	67-70	25-11	25-11	25-11	25-11	82-12
			US-10-092-750-45	-10-0	-10-0	-10-7	-10-2	-10-3	-10-4	-10-7	-10-4	-10-4	-10-4	-10-4	-10-2
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	DB	;	14	14	14	17	15	14	17	16	17	15	15	15	15
	Query		29	628	638	638	665	131	109	238	382	398	398	398	552
æ	Query Match		100.0	100.0	100.0	100.0	100.0	37.8	36.7	35.7	35.7	35.7	35.7	35.7	35.0
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	Result No.		-	~	c	4	S	9	7	80	6	10	11	12	13

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US-10-369-493-22933 US-10-282-122A-49861 US-10-424-599-191824 US-10-425-114-44618 US-10-425-114-44618 US-10-425-114-44618 US-10-425-114-44618 US-10-427-96200 US-10-282-122A-53145 US-10-369-493-260 US-10-369-493-260 US-10-369-493-263 US-10-369-493-263 US-10-369-493-263 US-10-369-493-263 US-10-369-493-263 US-10-408-765A-2181 US-10-425-115-365 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-765A-2181 US-10-408-768-118-281977 US-10-427-963-139454 US-10-322-238-12712	ALIGNMENTS 0092750 A1 ides Interactive with BCL ides/10/092,750 3-07 60/274,526 8 s Version 4.0	Score 143; DB 14; I Pred. No. 8.6e-14; O; Mismatches O; I AEIIERGIRQH 29
34.3 33.4 33.4 33.4 33.5 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6 33.6	Application US/1 Application US/1 Arrion. Philip W Arright, Julia Arright, Martin C ENTION: POLYPEPT ENTION: POLYPEPT ENTION: POLYPEPT CRITON NUMBER: US ATTON NUMBER	milarity 100.0% Conservative ALAYYSSRQYASALKHI
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RESULT 4

US-10-786-720-55

Sequence 55, Application US/10786720

Sequence 55, Application US/10786720

Sequence 55, Application Vo. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION: DISBASES

TITLE OF INVENTION NUMBER: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

NUMBER OF SEQ ID NOS: 21135

SEQ ID NO 55
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Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pena, Carol
Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 2099
LENGTH: 638
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Gerlach, Valerie
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Gorman, Linda
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Ji, Weizhen
                                                                                                          TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2099
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US-10-786-720-55
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                             APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE PATENTIN VOVER: 2.1
SEQ ID NO 3203
LENTH: 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 LALAYYSSRQYASALKHIAEIIERGIRQH 185
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR PILICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
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Publication No. US20030219741A1
GAPBRAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUGIYAMA, TOMOYASU
APPLICANT: OTSUGIYAMA, TOMOYASU
APPLICANT: STGO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HSONO, YUUKO
APPLICANT: HSONO, YUUKO
                                                        WAKAWATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAWAWOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                            NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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OTSURA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
OTSUKA, MOTOYUKI
        SUGIYAMA, TOMOYASU OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                        OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-094-749-3203
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US-10-425-115-276504
US-10-425-115-276504

US-10-425-115-276504

Sequence 276504, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 276504

LENGTH: 109
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Publication No. US20040172684A1
Publication No. US20040172684A1
Publication No. US20040172684A1
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21 (5335) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 32647
LENGTH: 238
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                                                                                                                                                                    Indels 30; Gaps
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                                                                                                Score 54; DB 14; Length 131; Pred. No. 5.5; 7; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_183754C.1.pep
US-10-425-115-276504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.7%; Score 52.5; DB 17; Best Local Similarity 35.7%; Pred. No. 7.5; Matches 10; Conservative 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(109)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LAYYSSROYASALKHIAEIIERG-IROH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 IRHHHMRQYVPALSHLSMVYPHGFLRQH 95
                                                                                                                                                                                                                                        1 LALAYYSSRQYASALKHI-----
                                                                                                    Query Match 37.8%;
Best Local Similarity 22.4%;
Matches 13; Conservative
; ORGANISM: Aquifex aeolicus
US-10-369-493-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                        δ
                                                                                                    APPLICANT: Ellerman, Karen
APPLICANT: Bilerman, Karen
APPLICANT: Bilerman, Karen
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Hospie, David
APPLICANT: Lepley, Denise et al.
TITLE COF INVENTION: THEREFERITO POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOR
TITLE COF INVENTION: THEREFERICANT APPLICATION NUMBER: US/10/210,172
CURRENT APPLICATION NUMBER: 60/30.501
FRIOR PRING DATE: 2001-08-03
FRIOR APPLICATION NUMBER: 60/313,914
FRIOR PRING DATE: 2001-09-01
FRIOR PELING DATE: 2001-08-03
FRIOR PELING DATE: 2001-08-04
FRIOR PELING DATE: 2001-08-04
FRIOR PELING DATE: 2001-08-04
FRIOR PELING DATE: 2001-08-05
FRIOR PELING DATE: 2001-08-07
FRIOR PELING DATE: 2001-08-07
FRIOR PELING DATE: 2001-08-07
FRIOR APPLICATION NUMBER: 60/311,979
FRIOR APPLICATION NUMBER: 60/311,979
FRIOR APPLICATION NUMBER: 60/311,979
FRIOR APPLICATION NUMBER: 60/313,201
FRIOR APPLICATION NUMBER: 60/312,992
FRIOR APPLICATION NUMBER: 60/313,201
FRIOR APPLICATION NUMBER: 60/313,201
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FRIOR APPLICATION NUMBER: 60/313,201
FRIOR APPLICATION NUMBER: 60/313,201
FRIOR APPLICATION NUMBER: 60/313,201
FRIOR PELING DATE: 2001-08-17
FRIOR APPLICATION NUMBER: 60/312,992
FRIOR APPLICATION NUMBER: 60/312,992
FRIOR PELING DATE: 2001-08-17
FRIOR PELING DATE: 2001-08-17
FRIOR PELING DATE: 2001-08-17
FRIOR PELING DATE: 2001-08-17
FRIOR APPLICATION NUMBER: 60/313,901
FRIOR PELING DATE: 2001-08-17
FRIOR PELING DATE: 2001-08-17
FRIOR APPLICATION NUMBER: 60/312,992
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| Sequence 106, Application US/10169493
| Publication No. US20030233675A1
| Publication No. US20030233675A1
| APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| APPLICANT: Slater, Steven C. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION NUMBER: US 10/369, 493
| CURRENT APPLICANTION NUMBER: US 60/360, 039
| PRIOR FILING DATE: 2002-02-21
| NUMBER OF SEQ ID NOS: 47374
| SEQ ID NO 106
| LENDTH: 131
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; ORGANISM: Homo sapiens
US-10-210-172-74
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Matches 29; Conserv
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TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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                                                                                                                                    JULIONARION NO. 1920040214272A1
Sequence 281833, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dlants
TITLE OF INVENTION: Dlants
TITLE OF INVENTION: Dlants
TITLE OF INVENTION: Dlants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Co, Yongwin Shucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53395
LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 51; DB 17; Length 382; Best Local Similarity 50.0%; Pred. No. 51; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_20131C.1.pep
US-10-425-115-281833
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OTHER INFORMATION: Clone ID: 700451509_FLI.pep
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US-10-425-114-53395
; Sequence 53395, Application US/10425114
; Publication No. US20040034888A1
                         171 YSNPGYLDALKHITDLKEEG 190
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YSSROYASALKHIAEIIERG 25
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                        RESULT 9
US-10-425-115-281833
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RESULT 11

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Sequence 64162, Application US/10425114
| Sequence 64162, Application US/20040034888A1
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Liu, Jingdong
| APPLICANT: Screen, Steven E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
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| APPLICANT: Tabaska
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| Sequence 72211, Application No. US2004003488A1
| General Information No. US2004003488A1
| General Information No. US2004003488A1
| General Information No. US2004003488A1
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
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| APPLICANT: Tabas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: LIB3592-097-D6_FLI.pep
US-10-425-114-64162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 700428946_FLI.pep
US-10-425-114-72211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.7%; Score 51; 50.0%; Pred. No.
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APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 YSNPGYLDALKHITDLKEEG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 YSNPGYLDALKHITDLKEEG 205
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FILE REFERENCE: ELITRA. 134A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

FRIOR APPLICATION NUMBER: 60/191,078

FRIOR PILING DATE: 2000-05-23

FRIOR PELING DATE: 2000-05-23

FRIOR APPLICATION NUMBER: 60/207,727

FRIOR APPLICATION NUMBER: 60/207,727

FRIOR APPLICATION NUMBER: 60/207,727

FRIOR PILING DATE: 2000-05-26

FRIOR APPLICATION NUMBER: 60/230,335

FRIOR PILING DATE: 2000-09-09

FRIOR PILING DATE: 2000-09-09

FRIOR PILING DATE: 2000-09-09

FRIOR APPLICATION NUMBER: 60/242,578

FRIOR APPLICATION NUMBER: 60/253,625

FRIOR PILING DATE: 2000-10-23

FRIOR PILING DATE: 2000-12-22

FRIOR PELING DATE: 2000-12-22

FRIOR APPLICATION NUMBER: 60/267,636

FRIOR APPLICATION NUMBER: 60/267,636

FRIOR APPLICATION NUMBER: 60/267,636

FRIOR APPLICATION NUMBER: 60/267,636

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FRIOR APPLICATION NUMBER: 60/267,636

FRIOR PILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-06

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09

FRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                   Length 272;
                                                                                                                                                       10; Indels
                                                                                                Score 49; DB 14;
Pred. No. 68;
5; Mismatches 10
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                                                                                                                                                                                                                                         1 LALAYYSSRQYASALKHIAEIIERGI 26
                                                                                                                                                                                                                                                                                                                                                                                Sequence 49861, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 ROYASALKHIAEIIERGIR 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Burkholderia fungorum
                                                                                                Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Kardt
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
; TYPE: PRT
; ORGANISM: Aeropyrum pernix
US-10-369-493-22933
                                                                                                                                                                                                                                                                                                                                                                .10-282-122A-49861
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Publication No. US20030233675A1

GENERAL INRORMATION:

APPLICANT: Cao, Yorgwei

APPLICANT: APPLICANT: Gregory J.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, WINTEN: BARRSSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (5.05.2) B

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/3-22

PRIOR APPLICATION OF SEQ ID NOS: 47374

SEQ ID NO 22933
                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Listeria monocytogenes
US-10-282-122A-60515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 YASDLSHIAEFGEKGV 190
                                            Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 YASALKHIAEIIERGI 26
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Best Local Similarity
Matches 10; Conserv.
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Gaps
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Query Match 34.3%; Score 49; DB 15; Length 380; Best Local Similarity 63.2%; Pred. No. 99; Matches 12; Conservative 1; Mismatches 4; Indels
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Job time : 34.5915 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53 ; Search time 7.11321 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-45 143 1 LALAYYSSRQYASALKHIABIIERGIRQH 29 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

.PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	1.5	ij	$\sim$	hypothetical prote	hetic	protein	protein -	replication protei	Na+/Pi-cotra	hypothetical prote	protein F5011.2 [i	hypothetical prote	н	hypothetical prote	a,	ical	tre	hypothetical prote	tetratricopeptide	. ന	competence protein		g	Ļ	tra	probable transposa			conserved hypothet
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	atch Length	18	131	368	1227	280	381	388	403	550	555	572	316	305	338	555	555	272	547	296	672	691	691	691	729	221	224	224	145	276
	Match	m	37.8	7.	ġ	ď.	ů.	ď.		ů	'n	ů.	ñ,	35.0	ū,	'n.	'n.	4.		4.	4.	4.	٠	4.	4.	ش	33.9	ω,	33.6	33.6
	Score	76	54	53	52	51	51	51	51	51	51	51	50.5	20	20	20	20	49	49	49	40	49	49	49	4	•	œ	٠	48	48
	No.		73	æ	4	S	9	7	80	σ		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

hypothetical prote	conserved hypothet	Ca2+/calmodulin-de	Ca2+/calmodulin-de	Ca2+/calmodulin-de	calcium-dependent	hypothetical prote	conserved hypothet	probable helicase	probable RNA-direc	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	sensory transducti	replication protei
E72564	C70124	A53036	TVRTC4	152637	A43713	T03427	AF3244	875377	S58380	E85082	T14186	B72236	B75153	875132	JQ1025
73	н	н	Н	N	-	7	~	N	~	7	N	~	7	~	7
277	379	473	474	502	508	527	550	875	2517	382	382	206	301	368	386
33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33,2	33.2	32.9	32.9	32.9	32.9
48	48	48	48	48	48	4.8	48	48	48	47.5	47.5	47	47	47	47
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1  P87767  Portion 1  P87767  Portion 2  Portion 2  Portion 3  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Cispedies: Caenorhabditis elegans  Rianonymous, F87767  Rianonymous, F87767  Rianonymous, F8776000, MUID: 99069613; PMID: 9851916  Aire ference number: A76000, MUID: 99069613; PMID: 9851916  Aire es websites genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ Aire es websites appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Aire elegans: preliminary  Aire elegans: Pype: DMA  Aire elegans: 1-418  Aire elegans: Caenorhabditis elegans: Aire elegans: Caenorhabditis elegans: Aire elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis elegans: Caenorhabditis eleg
Query Match 53.1%; Score 76; DB 2; Length 418; Best Local Similarity 51.7%; Pred. No. 0.0037; Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
OY 1 LALAYYSSRQYASALKHIAEIIERGIROH 29 
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove V. Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300: MIID:98196666: PMID:9537320
A;Accession: F70422 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-131 <aqf> A;Residues: 1-131 <aqf> A;Cross-references: UNIPROT:067408; GB:AE000739; NID:g2983813; PIDN:AAC07377.1; PID:g2983.</aqf></aqf>
C,Genetics: A,Genetics: A,Genetics: C,Superiment and 1409 C,Superiment and 1409 F;43-76/Domain: tetratricopeptide repeat homology <ttl> F;77-110/Domain: tetratricopeptide repeat homology <ttl></ttl></ttl>

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C;Accession: C64471
C;Accession: C6471
C;Cotton, L7;FlexCondition
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
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C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
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C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C64471
C;Cotton, L7;Accession: C6471
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C)Species: Lactococcus lactis
C)Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C)Date: 10-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C)Date: 10-Jan-1995 #sequence_revision: 840051, Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Novel, M.; Nove
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A, Residues: 1.381 <SEE>
A, Cross-references: UNIPROT: 048703; EMBL: 225477; NID: 9401838; PIDN: CAA80966.1; PID: 940183
C, Superfamily: Lactococcus lactis replication protein repB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
XResidues 1-288 FRES
A;Cross-references: UNIRROT:048681; EMBL:X60454; NID:g414894; PIDN:CAA42983.1; PID:g41486
C;Superfamily: Lactococcus lactis replication protein repB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-280 < BUL
A; Cross-references: UNIPROT: QS8767; GB: U67577; GB: L77117; NID: G2826400; PIDN: AAB99380.1;
C; Genetics:
A; Map position: FOR1320764-1321606
A; Start codon: GTG
C; Superfamily: conserved hypothetical protein YBR002c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CiSpecies: Lactococcus lactis
CiDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
CiDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
Risegers, J.F.M.L.; Franke, C.; Venema, G.; Bron, S.; Kiewiet, R.
submitted to the EMBL Data Library, August 1993
A;Description: The majority of lactococcal plasmids belong to one family.
A;Reference number: 837169
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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10;
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(7)
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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
35.7%; Score 51; DB
Best Local Similarity 40.0%; Pred. No. 10;
Matches 10; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 IAIAYGGQQEIIDAVKKIAEKVKRG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LALAYYSSRQYASALKHIAEIIERG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repB protein - Lactococcus lactis
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Best Local Similarity 33.3%;
Matches 9; Conservative 1.
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S40057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-368 <HEL>
A;Cross-references: UNIPROT:Q9KT55; GB:AE004186; GB:AE003852; NID:g9655507; PIDN:AAF9420
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response regulator VC1050 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Woleclut type: DNA
A;Rosidues: 1-1227 AEBV-
A;Cross-references: UNIPROT:Q9LXF4; EMBL:AL353993; GSPDB:GN00063; ATSP:F8M21.170
A;XXperimental source: cultivar Columbia; BAC clone F8M21
C;Genetics: A;Gene: ATSP:F8M21 110
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                                                                                                                                                                                                                                                                                            -----AEIIERGIRQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Sjecies: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A62249
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                                                                                                                                              30; Gaps
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                                                          Length 131;
                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 368;
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                                                     Score 54; DB 2;
Pred. No. 1.7;
7; Mismatches
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Pred. No. 6.9;
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                                                                                                                                                                                                                                           1 LALAYYSSRQYASALKHI--
                                                ch 37.8%;
1 Similarity 22.4%;
13; Conservative 7
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ilarity 61.1%;
Conservative
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Best Local Similarity
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                                                               Query Match
Best Local S
Matches 13
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Genetics:

Matches

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C., C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Kooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                          hypothetical protein AGR C 4085 [imported] - Agrobacterium tumefaciens (strain C58, Ceres C, Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens 03-Sep_20101 #sequence_revision 30-Sep_2001 #text_change 09-Jul-2004 C; Accession: B97629 R; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 #sthogen and Biotechnology Agent Agrobacterium tumefacence number: A97359; WUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q8UD82; GB: AE007869; PIDN: AAK87987.1; PID: g15157399; GSPDB: G
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86257
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C,Species: Sulfolobus solfataricus
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Pred. No. 21;
6; Mismatches 11; Indels
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Pred, No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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A;Gene: AGR C 4085
A;Map position: circular chromosome
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                                                408 YAINLEHIGDIIEKGI 423
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62.5%;
            YASALKHIAEIIERGI 26
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Best Local Similarity 32.0%;
Matches 8; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
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A,Molecule type: DNA
A,Residues: 1-555 <KUR>
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A,Molecule type: DNA
A,Residues: 1-572 <STO>
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AD2852
Na+/Pi-cotransporter Atu2245 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11.Jan-2002 #sequence_revision 11.Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2852
C;Accession: AD2852
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               At the Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

At Accession: AD2852
At Status: preliminary
At Status: preliminary
At Molecule type: DNA
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
At Status: 1-550 (CMR)
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Spides replication protein repB - Lactococcus lactis
C;Species: Lactococcus lactis
C;Species: Lactococcus lactis
C;Species: Lactococcus lactis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37168, 484976
R;Seegers, J.; Franke, C.; Venema, G.; Bron, S.; Kiewiet, R.
R;Description: The majority of lactococcal plasmids belong to one family.
A;Reference number: S37168
A;Reference number: S37168
A;Recession: S37168
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-403 <SEE.
A;Cross-references: UNIPROT:Q48701; EMBL:Z25475
B;Seegers, J.; Franke, C.; Venema, G.; Bron, S.; Kiewiet, R.
S;Description: The majority of lactococcal plasmids belong to one family.
A;Reference number: S44976
A;Reference number: S44976
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 19-403 <SE2.>
A;Cross-references: EMBL:Z25475; NID:g452758; PIDN:CAA80964.1; PID:g452759
C;Genetics:
A;Gene: repB
C;Superfamily: Lactococcus lactis replication protein repB
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35.7%; Score 51; DB 2; Length 403;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 9; Conservative 11; Mismatches 7; Indels
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                                      Indels
                                      7;
33.3%; Pred. No. 14; tive 11; Mismatches
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                                                                                          3 LAYYSSRQYASALKHIAEIIERGIRQH 29
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C,Ganetics:
A,Gene: Atu2245
A,Map position: circular chromosome
                                   9; Conservative
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Query Match
Best Local Similarity
Matches 10; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-338 <STO>
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C) Species: Bacillus subtilis
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C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: H90458
R; She, O; Singh, R.K; Confalonieri, F; Zivanovic, Y; Allard, G; Awayez, M.J.; Chan-Jong, I; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Abescription: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: H90458
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:Cross-references: UNIPROT:P54592; GB:299108; GB:AL009126; NID:92633055; PIDN:CAB12736
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C;Species: Bacillus halodurans
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C,Superfamily: ATP-binding cassette homology
C,Keywords: ATP; nucleotide binding; P-loop
F;20-209/Domain: ATP-binding cassette homology <ABC>
F;37-44/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 2;
Pred. No. 15;
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Pred. No. 14;
7; Mismatches
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Best Local Similarity 50.0%;
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Best Local Similarity 40.6
Matches 13; Conservative
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hypothetical protein lmo1434 [imported] - Listeria monocytogenes (strain EGD-e) (Species: Listeria monocytogenes (Species: Listeria monocytogenes (Species: Listeria monocytogenes (Species: Listeria monocytogenes (Species: Listeria monocytogenes (Species: Listeria monocytogenes (Spaces 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (Spaces 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (Species: Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguaz-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Dominguaz-Bernal, G.; Buchaud, L.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001 A.; Kunn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; A.; Mathors: Kreft, J.; Kunnst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mathand, A.; Mathors: Anderence number: AB1077; Muid:21537279; PMID:11679669 A.; A.; Voss, H.; Wehland, A.; A.; Mathors: Preliminary A.; Muid: M.; Mathors: A.; Mathors: A.; Mathors: Mathors: Mathand, A.; Mathors: Effect and A.; Mathors: Mathand, A.; Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathors: Mathor
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K,IAkami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A;Reference number: A83650; MUID:20512582; PMID:11058132
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01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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illarity 62.5%; Pred. No. 29;
Conservative 2; Mismatches
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Pred. No. 17;
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10; Conservative 9
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es 10; Conserv
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us-10-092-750-45.rup

GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 13:38:57 ; Search time 38.6302 Seconds (without alignments)

431.938 Million cell updates/sec

Title: US-10-092-750-45
Perfect score: 143
Sequence: 1 LALAYYSSRQYASALKHIAEIIERGIRQH 29

Sequence: 1 LALAYYSSRQYASALKHIAEI)
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_02:\* 1: uniprot\_sprot:\* 2: uniprot\_trembl:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	рошо		homod	homo	mus 7		Q9cy00 mus musculu	Ofinu8 xenopus lae	-							Q8pbp5 xanthomonas		dictyost									T	7	4 arab	57 mus	Q8cid2 mus musculu
SUMMARIES	ID	Q96NE6	Q8IVP2	Q8N4P2	Q86WI1	Q8C0X1	Q99J38	O9CY00	QGINU8	AAH72174	Q7PRA4	Q9VK41	Q817G3	Q817G4	Q9WWB1	067408	Q8PBP5	Q8PNA0	Q8MN61	Q7QVV8	Q7MIU6	Q8DB27	Q9KT55	Q8PSM9	Q7N0T3	THSB_SULAC	Q8T0 <u>2</u> 0	Q9W3Y6	AAF46175	Q9LXF4	Q9DA67	Q8CID2
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NEDLINE=22388257; PubMed=12477332;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Aptichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hillaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Galimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1018_TaxID=9606;
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TISSUB-Brain;
TISSUB-Brain;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033795; AAH33795.1; -.
EMBL; BC033795; PR009940; Prenyl_trans.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
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                                                                                                  (TremBirel. 22, Created)
(TremBirel. 22, Last sequence update)
(TremBirel. 26, Last annotation update)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LALAYYSSRQYASALKHIAEIIERGIRQH 29
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                                    PRT;
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SMART; SM00028; TPR; 4.
PROSITE; PS50293; TPR_REGION; 2.
                                    PRELIMINARY;
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                                                                                                  01-OCT-2002 (TrEMB)
01-OCT-2002 (TrEMB)
01-MAR-2004 (TrEMB)
FLJ30990 protein.
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Q8N4P2
ID Q8N4P2
AC Q8N4P2;
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Q86WT1
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                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                        Length 638;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC042848; AAH42848.1;
Interpro; IPR008940; Prenyl trans.
Interpro; IPR001440; TPR.
Interpro; IPR008941; TPR-like.
Pfam; PPF00515; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS50293; TPR REGION; 1.
Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 665 AA; 76177 MW; DC44E17689642854 CRC64;
       73146 MW; 16AB964E71ACF893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 und mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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100.0%; Score 143; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 29; Conservative 0; Mismatches 0;
                                                                     ; Score 143; DB 2;
; Pred. No. 6.1e-12;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           665 AA
                                                                                                                                                                                                                                                       194 LALAYYSSROYASALKHIAEIIERGIROH 222
                                                                                                                                                                                                           1 LALAYYSSRQYASALKHIAEIIERGIRQH 29
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                                                                        100.0%;
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Best Local Similarity 100...
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       638 AA;
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MEDLINE=21085660; PubMed=11217851;
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                                                                                             Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Widin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
M. Mandan A., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
M. Mandan A., Smailus D.E., Schnerch A., Schein J.E.,
M. Marra M.A.,
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M. Mandan A., Mandan A., Schein B.D., Dickson M.C.,
M. Madan A., Mandan A., Schein B.D., Dickson M.C.,
M. Mandan A., Schein B.D., Marra M.A.,
M. Mandan A., Smailus D.E., Schnerch A., Schein J.E.,
M. Mandan A., Schein B.D., Marra M.A.,
M. Mandan A., Smailus O., Mandan A., Schein J.E.,
M. Mandan A., Schein B.D., Marra M.A.,
M. Mandan A., Schein B.D., Marra M.A.,
M. Mandan A., Schein B.D., Mandan A., Schein J.E.,
M. Mandan A., Schein B.D., Mandan A., Schein J.E.,
M. Mandan A., Schein B.D
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-0CT-2003 (TrEMBLRel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone-1921518C04 product:hypothetical Tetratricopeptide
repeat (TRN) structure containing protein, full insert sequence.
Name=4930506L13Rik;
Mus musculus (Mouse).
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=99279253; PubMed=10349636;
                                      TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932;
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STRAIN=C57BL/6J; TISSUE=Testis;
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STRAIN=C57BL/6J; TISGUE=Testis;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,
A Huyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishili Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Saaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
I Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            SEQUENCE FROM N.A.
STRANIESTSBL/607 IISSUE=Testis;
The FANTOM CONSORtium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Habata N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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MEDLINE=CS7BL/GJ; PLOMEd=11076861;

MEDLINE=CS7BL/GJ; PubMed=11076861;

MEDLINE=CS7BL/GJ; PubMed=11076861;

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Marsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Marsumas S., Kawai J., Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Sequencing pipeline with 384 multicapillary sequencer.";
                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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93.1%; Pred. No. 9.2e-11;
ive 1; Mismatches 1; Indels
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Hypothetical protein; Repeat; TPR repeat.

SEQUENCE 664 AA; 76221 MW; 70FA38E48D95F3AS CRC64;
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InterPro, IPR001440; TPR.
InterPro, IPR008941; TPR-like.
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Best Local Similarity 93.15
Matches 27; Conservative
RIKEN FANTOM Consortium;
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SMART; SM00028; TPR; 4.
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ID Q99J38
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[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
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STRANN=CS7BL/6J; TISSUB=Parthenogenote;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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         01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2004 (TrEMBLrel. 18, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
RIKEN CDNA 4930506131 (Wus musculus 9.5 days embryo parthenogenote CDNA, RIKEN full-length enriched library, clone:B130032F08
product:Mypothetical Tetratricopeptide repeat (TPR) structure containing protein, full insert sequence).
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NMRI, TISSUE=Mammary tumor. WAP-Tag model. 5 months old, Strausberg R., Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUB=Parthenogenote; MEDLINE=99279253; Pubmed=10349636; Carninci P., Rayashizaki Y.; Hidh-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUB=Parthenogenote;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                            Mus musculus (Mouse).
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                                                                                                                                                                    NCBI_TaxID=10090;
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STRAIN-CSPEL/67, TISSUB-Parthenogenote;
A dachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Hara A., Hashizume W., Puruno M., Hangaki T., Hara A., Hashizume W., Hayashida K., Hayasuu M., Hirancto K., Hiracka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katai J., Kojima Y., Konno H., Kodno H., Kodna M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakazume N., Sano H., Saski C., Shinata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Takawa A., Tak
P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=C57BL/6J; TISSUE=Parthenogenote;

STAIN=C57BL/6J; Pubmed=11076861;

X MEDLINE=20530913; Pubmed=11076861;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., A Fuliwake S., Inoue K., Togawa K., Izama M., Ohara E., Watahiki M., Yoneda Y., Narama T., Oazawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rapu T., Matsuura S., Kawai J., Rapuna J., Saguencing pipeline with 384 multicapillary sequencer.";
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01-UTM-2001 (TYEMBLEE]. 17, Created)
01-UTM-2001 (TYEMBLEE]. 25, Last sequence update)
01-OCT-2003 (TYEMBLEE]. 25, Last annotation update)
101-OCT-2003 (TYEMBLEE]. 25, Last annotation update)
11-OCT-2003 (TYEMBLEE]. 25, Last annotation update)
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthezia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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76237 MW; F9C3C7863231CEA2 CRC64;
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STRAIN=C57BL/60; IISSUB=Liver;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 664 AA; 76237 MW; F9C3C78632
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InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 4.
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Xenopus laevis (African clawed frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cvary;
MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC072174; AAH72174-1; -.
InterPro; IPR001440; TPR. InterPro; IPR001440; TPR. InterPro; IPR001541; TPR. 2.
SMART; SM00028; TPR; 4.
PROSITE; PS50005; TPR; 1.
PROSITE; PS500293; TPR; 1.
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SEQUENCE 651 AA; 75558 MW; AF0608F6F7986590 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
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                                                           MGC80272 protein.
Name=MGC80272;
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01-JUN-2004 (
01-JUN-2004 (
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ID AAH7
AC AAH7
DT 01-J
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SEQUENCE FROM N.A.
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A motani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A matsuyama T., Miyazaki A., Nishi K., Nomura K., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakai K., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
A Fejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Lumansu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, MGI:1919671; 2510042P03Rik.
                                                                            [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
The FANTOM Consortium,
the RANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
whallysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                     STRAIN=CSTBL/6J; TISSUB=Liver;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRIN=C57BL/6J; TISSUE=Liver;

STRIN=C57BL/6J; TISSUE=Liver;

MEDLINE=2039013; PubMed=11076861;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama M., Aisawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunco H., Sakaquchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wathiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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SEQUENCE 664 AA; 76095 MW; 8BCB2D1F1A7099F3 CRC64;
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  MEDLINE=21085660; PubMed=11217851;
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E; PS50293; TPR_REGION; 1.
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InterPro; IPR008941; TPR-like.
Pfam; PF00515; TPR; 3.
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Matches 27; Conservative
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                      RIKEN FANTOM Consortium;
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Gaps

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Q6INU8
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Length 651; Indels . 0

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preliminary data.

EMBL, AAAB01008859; EAA07585.2;
Interpro; IPR001440; TPR.

PROSITE; PS50005; TPR; I.

PROSITE; PS50293; TPR_REGION; I.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                         15; Conservative
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STRAIN=PEST
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SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
            Hypothetical protein.

Hypothetical protein.

Hypothetical pavis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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75.9%; Pred. No. 2.6e-08;
ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC0721174.1; -.
Hypothetical protein.
SEQUENCE 651 AA; 75558 MW; AF0608F6F7986590 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENSANGP00000024665 (Fragment).
Name=ENSANGG00000020924;
                                                                                  Kenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                        Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Ovary;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                NCBI TaxID=8355;
                                                                                                                                                                                                           Richardson P.;
                                                                                                                                                         IISSUE=Ovary;
                                                                                                                                                                                                                                           initiative.
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[1] SEQUENCE FROM N.A.

Q7PRA4 RESULT 10 Q7PRA4

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REDLINE=20196006; PubMed=10731112;

RADRES RAD, Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Batton G.G., Mortman J.K., Yandell M.D., Zhang O., Chen L.X.,

RA Abril J.F., Agapayari A., An H.J., Andrews P. Fannkoch C., Baldwin D.,

RA Abril J.F., Agapayari A., Rareja R.G., Champe M., Pfelifer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Banadari D., Belshakov S.,

RA Ballew R.M., Basu A., Barendel J., Banadari D., Bolshakov S.,

RA Ballew R.M., Basu A., Barendel J., Banadari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Gebric B. Delcher A., Dahlke C., Davenport L.B. Davets P.,

RA Gebric B. Delcher A., Dahlke C., Perriera S., Ferise R.M.,

RA Harris N.L., Harvay D., Helman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Harvy D., Helman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Marvy D., Helman T.J., Herrandez J.R., Houck J.,

RA Jallin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum K.A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

RA Merkilov G., Milshian N.V., Nobarry C., Morris G., Kulp D., Lai Z.,

RA Alazolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Resee M.G.,

RA Adier R., Ratcher R.A., Nobarry C., Morris G., Pull J., Moshrefi A.,

RA Menner S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nobleon D.K.,

RA Shines R., Tector C., Trinet R., Venter E., Wang R., Shib T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Shireks R., Tector C., Triner R., Venter E., Wang A., Weller R., Wenley R.,

RA Shireks R., Tector C., Triner R., Venter E., Wang A., Welley R.,

Rand R., Wenley R., Millen R., Welley R., Welley R.,

Rand R., Wenley R.,
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endobrerygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, NGEL TaxID=7227;
                                                                                                                                                                                                                                                                                                                                Length 634;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                               634 AA; 69956 MW; 7954B31DDE29C4DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                56.6%; Score 81; DB 2;
53.6%; Pred. No. 0.006;
tive 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 ALCHYRKENSQALNYIAEIVERGIRNH 194
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Name=F54C1.5;
Caenorhabditis elegans.
Ebukaryota, Metacoa, Nemacoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
Miller N., Bradshaw H., Wamsley P.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENEL; U88165; AA012421.1; --
WormPep; F54C1.5b; CE33109.
InterPro; IPR001440; TPR.
InterPro; IPR00841; TPR-like.
PROSITE; PS02033; TPR_REGION; 1.
Hypothetical protein.
SEQUENCE 597 AA; 68565 MW; ADFC80974415DC74 CRC64;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F54C1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 51.7%; Score 76; DB 2;
Conservative 5; Mismatches
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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MEDLINE=99069613; PubMed=9851916;
Wilson R.;
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                                                                                              Name=F54C1.5;
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                            NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                          Wilson R.;
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                                                                                                                           MEDINES-21466065, PubMed=12537568;
MEDINES-22466065, PubMed=12537568;
MEDINES-22466065, PubMed=12537568;
MEDINES-22466065, PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patk S., Pefiffer B.D., Richards S., Sodergren E.J.,
Weinskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchrcmatic genome sequence.",
           Zheng L.,
Zhu X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Partel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22456069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003638; AAF53241.1; -
FYBase; FBGN0032470; CG5142.
GO; GO:0003700; Fitznascription factor activity; IEA.
GO; GO:0006355; Piregulation of transcription, DNA-dependent; IEA.
InterPro; IPR00197; HTH Fis.
InterPro; IPR001440; TPR.
InterPro; IPR008941; TPR-like.
PF00515; TPR; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%; Score 78; DB 2; Length 652; 48.3%; Pred. No. 0.017; 7; Indels tive 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLYBASE;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EA71A55AA1350266 CRC64;
  Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Prosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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PROSITE; PS50005; TPR; 1.
SEQUENCE 652 AA; 72611 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.33
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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FLYBASE

Q817G3 Q817G3; RESULT 12 Q817G3 ID Q817G3 AC Q817G3

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Gaps

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Length 597; Indels

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374 YATNLEHIGDIIEKGLLQ 391
            11 YASALKHIAEIIERGIRQ 28
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067408
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STRAIN=Chry5;
Oger P.M., Farrand S.K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055246; AADJ1607.1; -.
EMBL; AF055890; C:membrane; IEA.
GO; GO:0005817; P:phosphate transport; IEA.
InterPror, IFR003841; Na/Pi_cotranspt.
Ffam; PF05690; Na Pi_cotrans; 1.
TIGRFAMS; TIGR01013; 2258.1;
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investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
BMB.; U88165; AAQ12420.1;
WormPep; F54C1.5a; CE33108.
InterPro; IPRO0941; TPR.
InterPro; IPRO0941; TPR-1ike.
SMART; SM00028; TPR; 3.
PROSITE; PSS0293; TRR_REGION; 1.
Hypothetical protein.
                                                                                     SEQUENCE FROM N.A.
STRALM-Bristol N2;
Miller N., Fardshaw H., Wamsley F.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAND-Bristol N2;
Waterston R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ'databases
                                                                                                                                                                                                                                                                                                                                                                                 Wilson R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 AA; 55197 MW; 563AF8A98BAEFB8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.1%; Score 76; DB 2;
Best Local Similarity 51.7%; Pred. No. 0.033;
Matches 15; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LALAYYSSRQYASALKHIAEIIERGIRQH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Creat 01-NOV-1999 (TrEMBLrel. 12, Last 01-OCT-2003 (TrEMBLrel. 25, Last Hypothetical protein (Fragment). Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Plasmid.
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   [5]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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MEDLINE=S0196666; PubMed=9537320;
MEDLINE=S0196666; PubMed=9537320;
Graham D.E., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                    Aquifex aeolicus.
Bacteria, Aquificae, Aquificales, Aquificaceae, Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature 392.353-358(1998).

BMBL; AB000739; AAC07377.1; -.

PIR; PF0422; PF0440;

IN CAPPO; IPR001440;

InterPro; IPR008941; TPR.

InterPro; IPR008941; TPR.

Pfam; PF06515; TPR; 2.

PROSITE; PS50005; TPR; 1.

PROSITE; PS5023; TPR REGION; 1.

COMplete Protecome; Hyporhetical protein.

SEQUENCE 131 AA; 15774 MW; 49E428E0D8580709 CRC64;
                                                                         01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein aq 1409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.8%; Score 54; DB 2;
22.4%; Pred. No. 10;
iive 7; Mismatches
  131 AA
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                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
  PRT;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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; Search time 13.9094 Seconds (without alignments)
181.178 Million cell updates/sec US-10-092-750-46 210 1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTPHPPHS 38 November 10, 2004, 13:44:14 OM protein - protein search, using sw model Perfect score: Run on: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

478139 segs, 66318000 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
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/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ш		Query					
No.	Score	Match	Length	BB	ΠD	Description	
н	57.5	27.4	112	4	-09-270-767-4655	equence 465	<b>ا</b> ا
0	26	ú	33	4	-09-543-681A-47	753	ρ
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21	20	۳.	64	4	US-09-418-963-2	, Ap	٠,
22	4	e,	13	4	-09-270-767-4	1247	A
23	4	w.	13	4	-09-270-767-564	6463	Ø
24	49	m	1	4	-09-621-976-	Sequence 7078, Ap	Q
25		'n.	19	4	-09-328-352-466	665,	Ω
92	49	· ·	51	4,	-09-257-825B-	1, A	,—
27		23.3	m	4,	-09-543-681A-5	538	ρ

	Sequence 1289, Ap	Sequence 2, Appli	Sequence 2, Appli	7	Sequence 8, Appli	2,	10,	1370,	Sequence 9445, Ap	20,	Sequence 35, Appl	'n	Sequence 2, Appli	64	48	32	Sequence 16, Appl
US-08-227-536-2	US-09-538-092-1289	PCT-US95-04682-2	US-08-194-468-2	US-08-961-739-2	US-09-514-247A-8	US-09-686-316-2	US-09-514-247A-10	US-09-538-092-1370	US-09-489-039A-9445	US-09-257-825B-20	US-09-028-934-35	US-07-727-814B-2	US-08-258-614-2	US-09-854-856-64	US-09-854-856-48	US-09-854-856-32	US-09-854-856-16
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28			31		33	34	.35	36	37	38	39	40	41	42	43	44	4.5

### ALIGNMENTS

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Sequence 46552, Application US/09270767
Patent No. 6703491
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Patent No. 6703491
Patent September: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
PURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
PATENT: LIANGE CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTINUED CONTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.4%; Score 57.5; I
Best Local Similarity 35.3%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-46552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Drosophila melanogaster FEATURE:
US-09-270-767-46552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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US-09-543-681A-4753

US-09-543-681A-4753

Sequence 4753, Application US/09543681A

Sequence 4753, Application US/09543681A

Sequence 4753, Application US/09543681A

Sequence 47510

TITLE NO. 6605709

TITLE OF INVENTION: UNGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL.

TITLE OF INVENTION: UNWHER: US/09/543,681A

CURRENT RAPLICATION UNMER: US/09/543,681A

CURRENT RAPLICATION NUMBER: US/09/543,681A

PRIOR APPLICATION NUMBER: US/09/2406

PRIOR PILING DATE: 2000-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 4753

LENGTH: 334

TYPE: PRT

TYPE: PRT

CREAM: Proteus mirabilis

US-09-543-681A-4753

DB 4; Length 334; 26.7%; Score 56; Query Match

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US-0-3-40-0-204-305

Sequence 55, Application US/09340620A

Patent No. 6482933

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC

FILE REPERRNCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT FILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1998-12-06

PRIOR PAPLICATION NUMBER: US 09/09,041

PRIOR PLING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

SOFTWARE FILING DATE: 1998-22-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE FALSES FARSES FOR Windows Version 4.0
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APPLICANY: XIAO, BO
APPLICANY: LEAHY, Daniel
APPLICANY: LEAHY, Daniel
APPLICANY: LEAHY, Daniel
APPLICANY: LEAHY, Daniel
APPLICANY: LEAHY, Daniel
APPLICANY: LANAHAN, Anthoray
APPLICANY: LANAHAN, Anthoray
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1D PROTEIN (AS AMENDED)
FILE REFERENCE: JUHISBO-4
CURRENT APPLICATION NUMBER: US 60/138,426
FRIOR APPLICATION NUMBER: US 60/138,493
FRIOR APPLICATION NUMBER: US 60/138,494
FRIOR APPLICATION NUMBER: US 60/138,494
FRIOR APPLICATION NUMBER: US 60/037,334
FRIOR APPLICATION NUMBER: US 60/097,334
FRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VEFFION 3.0
SEQ ID NO 44
FRIOR FILING DATE: 1998-08-18
SEQ ID NO 44
FRIOR FILING DATE: 1998-08-18
SEQ ID NO 44
FRIOR FILING DATE: 1998-08-18
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Patent No. 6720175
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: WORLEY, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.8%; Score 52; DB 4; Le
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 6; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTP 33
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Best Local Similarity 32.4%; Pred. No. 26;
Matches 11; Conservative 9; Mismatches
10 DDGGRELLAWLREMRHHHPVHEDEYGAFH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
, ORGANISM: Homo sapiens
US-09-340-620A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TU, Jian
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LENGTH: 1037
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Patent No. 6673910
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3745
LENGTH: 219
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                                   Gaps
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APPLICANT: PARIS, Jean Marc
APPLICANT: DUTRIC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramine And Method For Preparing Same By
TITLE OF INVENTION: Mitasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765, 907A
CURRENT FILING DATE: 1997-03-20
SUFFWARE: PATENTIN VOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.8%; Score 52; DB 4; Length 219; 27.0%; Pred. No. 18; ive 5; Mismatches 13; Indels
                                Indels
                                   10;
        Best Local Similarity 48.0%; Pred. No. 8.2;
Matches 12; Conservative 3; Mismatches
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                                                                                                                               52 LDYRKPKSDQWINQTELLPPIAKDV 76
                                                                                         S LDRRGTECDLWINEMSLLHKIVQDV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THIBAUT, Denis APPLICANT: THIBAUT, Denis APPLICANT: THIBAUT, Denis APPLICANT: BAMAS-JACQUES, Nathalie APPLICANT: COUZET, Joel APPLICANT: COUZET, Joel APPLICANT: BERSERERE, Jean-Claude APPLICANT: BEBUSSCHE, Laurent APPLICANT: FAMECHON, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-765-907A-10
'Sequence 10, Application US/08765907A
'Setent No. 6352839
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 27.0°
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: M.catarrhalis
US-09-540-236-3745
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                                                                                                                                                                                                                                 RESULT 3
US-09-540-236-3745
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LENGTH: 399
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Pred. No. 74;
4; Mismatches 8; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261B
FILING DATE: 0-JUN-1994
CLASSIFICATION NUMBER: US/08/258,261B
FILING DATE: US/08/258,261B
FILING DATE: US/08/258,261B
APPLICATION NUMBER: US/08/258,261B
APPLICATION NUMBER: US/08/258,261B
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELEPRANICATION INFORMATION:
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APPLICANT: Schubb, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Hammer, Phillip B.
APPLICANT: Hammer, Phillip B.
APPLICANT: Hammer, Phillip B.
APPLICANT: And Schoper Corp.
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: Antipathogenic substances
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 72
ADDRESSER: Ciba-Geigy Corporation
STREET: 7. Skyline Drive
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
FREFERENCE/DOCKET NUMBER: 38, 241
FREEDHOME: 919-541-8587
TELEPHOME: 919-541-8587
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE THE PROFESTION OF SEQ ID NO: 54:38; SCOTE 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.35
Thes 10; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 7 Skylin
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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Sequence 14868, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: WOLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14868
LENGHH: 298
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APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Hammer, Philip E.
APPLICANT: Hammer, Philip E.
APPLICANT: Warner, Sabine
APPLICANT: Wirner, Sabine
APPLICANT: Warner, Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: 37
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: NO. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
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Pred. No. 36;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
                                                                                                                               S LDRRGTECDLWIN-EMSLLHKIVQDVYGTPHPPH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.3%; Score 51; DB 4 Best Local Similarity 28.6%; Pred. No. 36; Matches 12; Conservative 5; Mismatches
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APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09028934
Patent No. 6117670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-09-028-934-31
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US-08-457-342-4; Sequence 4, Application US/08457342; Patent No. 5662898
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STREET: 7 Skylir
CITY: Hawthorne
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                                                           DB 1; Length 567; 74;
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                                                                                                        8; Indels
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/457,205
FILING DATE: 0-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: GC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE: 919-541-8649
INFORMATION FOR SEQ ID NO: 4:
SEQUIRNEE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James Joseph
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                              Score 51; DB 1
Pred. No. 74;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                             58 IPETSLMNRIIADRYGIPELDH 79
                                                                                                                                                16 INEMSLLHKIVQDVYGTPHPPH 37
                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08456837 Patent No. 5643774
                                                           Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.5
Matches 10; Conservative
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           ;
US-08-258-261B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-456-837-4
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45.5%; Pred. No. 74;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
PRICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATONREY/AGENT INPOMMATION:
NAME: ELMER' James SCOCT
REGISTRATION NUMBER: 36,129
APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,129
3R: CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                            : Ciba-Geigy Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 INEMSLLHKIVQDVYGTPHPPH 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08457646A Patent No. 5679560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKST NUMBER: CG
TELEPOWNUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                         COMPUTER: FLORDY disk

COMPUTER: PLORDY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:
PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,076A

FILING DATE: U-JUN 1995

CLASSIFICATION DATA:
PRILICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
BPLICATION NUMBER: US/258,261

FILING DATE: 01-JUN 1994

ATTORNEY/AGRAT INFORMATION:
NAME: Elmer, James Scott
RGISTATION NUMBER: 36,129

REPERRNCE/DOCKET NUMBER: GC 1506/CIP3

TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8614

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEGETAX: 919-541-8614

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEGETAT: 567 maino acids

LENGTH: 567 maino acids
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08457335A
Patent No. 5723759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 567 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-458-076A-4
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: USA

ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MG-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
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REFERENCE/DOCKET NUMBER: 36,129
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REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REPERENCE/DOCKET NUMBER: 36,129
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clare ADDRESS:
STREET: 7 Skyline Drive
GTTY: Hawthorne
GTTY: Hawthorne
STRATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Memory Scott Useeph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cipa-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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7 Skyline Drive
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Patent No. 5698425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMA
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US-08-729-214-4
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24.3%; Score 51; DB 1; Length 567;
Best Local Similarity 45.5%; Pred. No. 74;

Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
STATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Medisg, J. Timothy
REGISTRATION NUMBER: 38,241
RESPERIOC/OCKET NUMBER: CGC 1506/CIPS
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8689
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE: CHARACTERISTICS:
LEMOTH: 567 amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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Sequence 4, Application US/08729214

Batent No. 5817502

GENERAL INFORMATION:

APPLICANT: Ligon, James M.

APPLICANT: Hill, Dwight Steven

APPLICANT: Hill, Dwight Steven

APPLICANT: Hill, Dwight Steven

APPLICANT: Ryals, John Andrew

APPLICANT: Ryals, John Andrew

APPLICANT: Kirner, Phillip E.

APPLICANT: Kirner, Sabine

TITLE OF INVENTION: Genes for the synthesis of

TITLE OF INVENTION: antipathogenic substances

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation

STREET: 520 White Plains Road

CITY: TATTYCOWN

COTTY: TATTYCOWN
             CLASSIFICATION: 0.v.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE THARACTERISTICS:
LENGTH: 567 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 IPETSLMNRIIADRYGIPELDH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 INEMSLLHKIVQDVYGTPHPPH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
      CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-457-335A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-729-214-4
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Query Match

24.3%; Score 51; DB 2; Length 567;
Best Local Similarity 45.5%; Pred. No. 74;
Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                        Search completed: November 10, 2004, 14:55:34 Job time : 13.9594 secs
                                                                                                                                                                  58 IPETSLMNRIIADRYGIPELDH 79
                                                                                                                         16 INEMSLLHKIVQDVYGTPHPPH 37
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Sequence 8588, Ap Sequence 12153, Ap Sequence 12153, A Sequence 159959, Sequence 176444, Sequence 138825,

Sequence 15523, Sequence 10395, A Sequence 55, Appl Sequence 264527, Sequence 14, Appl Sequence 12524, Appl Sequence 1253, Appl Sequence 5, Appl Sequence 57, Appl Sequence 57, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 28, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appli Sequence 38, Appli

Sequence Sequence Sequence

score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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100.0%; Score 210; DB 14; Length 38; 100.0%; Pred. No. 2.4e-21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and supplication US/10092750
publication No. US20030032157A1
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpini, Julia
APPLICANT: Mright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US/2074,526
PRIOR PLING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 38
6 US-10-437-963-159960

5 US-10-35-977-8588

6 US-10-156-761-12153

6 US-10-437-963-159959

6 US-10-424-599-136444

6 US-10-437-963-136959

6 US-10-437-963-136959

6 US-10-437-963-136553

4 US-10-637-981-55

7 US-10-63-493-10395

8 US-10-295-981-55

10S-10-125-115-264527

10S-10-125-115-26841

10S-10-125-115-26841

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10S-10-68
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US-10-156-761-8999
Sequence 8999, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 38; Conservative
    TYPE: PRT
ORGANISM: Homo sapiens
  -10-092-750-46
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Sequence 8999, Ap
Sequence 608, App
Sequence 608, App
Sequence 127540,
Sequence 113540,
Sequence 188840,
Sequence 313042,
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Sequence 2206, Ap
Sequence 74677, A
Sequence 2115, Ap
Sequence 333859,
                                                                                                                              November 11, 2004, 01:28:30; Search time 43.9509 Seconds (without alignments) 305.399 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT TWEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT TWEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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210
1 AAMLDRRGTECDLWINEMSLLHKIVQDVYGTPHPPHS 38
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-092-750-46
US-10-156-761-8999
US-10-080-170-608
US-10-080-170-608
US-10-437-965-12540
US-10-437-96-12540
US-10-104-047-2206
US-10-104-047-2206
US-10-0847-2206
US-10-104-047-2215
US-10-0847-2215
US-10-0847-2215
US-10-0847-2215
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                                                                                                                                                                                                                                                                                                                                                 1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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1084
1084
1002
2010
2010
2010
303
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Gaps

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Score

Result

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SEO ID NO 127540
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US-10-468-356-608
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Sequence 608, Application US/10080170;
Publication No. US20030129601A1
GENERAL INFORMATION:
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT APPLICATION NUMBER: 60/270,123
FRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 608
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: OF MYCOBACTERIOSES
FILE REFERENCE: 03495,0218
CURRENT APPLICATION NUMBER: US/10/080,170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTPHP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AFILDRMSQOVDADEHRVALLRKTVGETWGLPSP 155
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Best Local Similarity 35.3%; Pred. No. 13;
Matches 12; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                   APPLICANT: ISHIKAWA, JUNA
APPLICANT: ISHIKAWA, JUNA
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
SPRIOR APPLICATION NUMBER: JP 2001-272697
SPRIOR SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.6%; Score 58; DB Best Local Similarity 37.1%; Pred. No. 61; Matches 13; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Sequence 608, Application US/10080170 ; Publication No. US20040121322A9 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptomyces avermitilis US-10-156-761-8999
OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-10-080-170-608
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US-10-080-170-608
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APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Wu, Wei Hei APPLICANT: Wu, Wei Hei APPLICANT: Wu, Wei Hei APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping APPLICANT: Li, Ping ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gequence 608, Application US/10468356

publication No. US20040197896A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 05394.0019

CURRENT FILING DATE: 2003-08-19

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: 06/270,123

PRIOR FILING DATE: 2001-02-22

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 655

SOFTWARE: Patentin Ver. 3.2

LENGTH 184
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27.1%; Score 57; DB 17; Length 184;
Best Local Similarity 35.3%; Pred. No. 13;
Matches 12; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                   Score 57; DB 16; Length 184;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                   Query Match 27.1%; Score 57; DB :
Best Local Similarity 35.3%; Pred. No. 13;
Matches 12; Conservative 7; Mismatches
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; Sequence 127540, Application US/10437963
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: AVAIL, David K.
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yorgwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION WUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 608
LENGTH: 184
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WS-10-106-698-5169

WS-10-106-698-5169

Sequence 5169, Application US/10106698

Publication No. US2033109690A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT FILING DATE: 2002-03-28

PRIOR FLING DATE: 2000-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

LENGTH: 275
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LOCATION: (1817)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KBY: MISC FEATURE
LOCATION: (1847)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KBY: MISC FEATURE
LOCATION: (2657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-5169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                       Length 210;
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Bublication No. US2003236392A1

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TILLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT APPLICATION NUMBER: 2002-03-25

PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
25.7%; Score 54; DB 14; Length 27
Best Local Similarity 34.1%; Pred. No. 52;
Matches 14; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MLLDRRGTECDL -- WINEM -- SLLHKIVQDVYGTPHPPHS 38
                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_48552C.1.pep
US-10-425-115-313042
                                                                                                                                                    Ouery Match 25.7%; Score 54; DB Best Local Similarity 52.9%; Pred. No. 39; Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                           22 LHKIVODVYGTPHPPHS 38
                                                                                                                                                                                                                                                                                      1 MHAYILDFYYTCHPPHS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-104-047-2206
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Bouldwarov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 188840
LENGTH: 1755
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US-10-425-115-313042

Sequence 313042, Application US/10425115

Sequence 313042, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REPERENCE 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 313042

LENGTH: 210
                                                                                                                                                                                                                                                                                                                                      ۲;
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                                                                                                                                                                                                                                                                                   DB 16; Length 102;
                                                                                                                                                                                                                                                                              Query Match

26.0%; Score 54.5; DB 16; Length
Best Local Similarity 24.3%; Pred. No. 15;
Matches 9; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29982C.1.pep
US-10-437-963-127540
                                                                                                                                                                                                                                                                                                                                                                                                                  14 LILDREASNGDVYTHHQNQIIESSAETLYGXMHPKHN 50
                                                                                                                                                                                                                                                                                                                                                                                    3 MLLDRRGTECDLWINEMS-LLHKIVQDVYGTPHPPHS 38
                                                                                                 NAME/KEY: unsure
LOCATION: (1)..(102)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1070 IWVGNNTALQHKLVNELHATPLGGHS 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 188840, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La APPLICANT: Kovalic, David K:
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                           TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-437-963-188840
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JAPLICAMIT. NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,335

PRIOR PELICATION NUMBER: 60/20,335

PRIOR PELICATION NUMBER: 60/20,335

PRIOR PELICATION NUMBER: 60/20,347

PRIOR PELICATION NUMBER: 60/20,347

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,365

PRIOR PELICATION NUMBER: 60/20,308

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PRIOR PELICATION NUMBER: 60/20,308

PRIOR PELICATIO
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Pred. No. 96;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 MLLDRRGTECDL --- WINEM -- SLLHKI VQDVYGTPHPPHS 38
                                                                                                                                                                                                                                                                                                        Query Match 25.7%; Score 54; DB 1
Best Local Similarity 34.1%; Pred. No. 88;
Matches 14; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-282-122A-74677

Sequence 74677, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant
Yamamoto, Robert
Forsyth, R.
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2206
LENGTH: 446
                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-2206
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DEWINEMSLIHKIVQDVYG 31

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Sequence 333859, Application US/10425115

Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Las Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Annualic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 1e+02;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_67590C.1.pep
US-10-425-115-333859
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
ITILE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 GTECDLWINEMSLLHKIVQDVYGTPHPP 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2.1
RESULT 12
US-10-094-749-2115
US-10-094-749-2115
; Sequence 2115, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
                                                                                                                                                                          WAKAWATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAWAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                          HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHICA, ICHIRO
SEKI, NAOHIKO
                                                                                                             APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.7%;
Best Local Similarity 39.3%;
Matches 11; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                          YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-094-749-2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
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Query Match 25.2%; Score 53; DB 15; Best Local Similarity 54.2%; Pred. No. 1.36+02; Matches 13; Conservative 3; Mismatches 6
                              ALICANAI, TAGEAL INFORMATIONS

RAME: MANDERAGOURSE, ANY E.

REGISTRATION NUMBER: 36, 207

REFERENCE/DOCKET NUMBER: 37, 207

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 724-214

INFORMATION FOR SEQ ID NO: 8588:

SEQUENCE CHARACTERISTICS:

LENGTH: 468 anino acids

TYPE: anino acid

TOPOLOGY: linear

MOLECULE TYPE: procein

HYPOTHETICAL: YES

ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...468
; SEQUENCE DESCRIPTION: SEQ ID NO: 8588:
US-10-335-977-8588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 11, 2004, 02:43:02 Job time : 45.0009 secs
                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 AMLFDRNGVETECDLKVDCKELLN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AMLLDRRG--TECDLWINEMSLLH 23
FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               FEATURE
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.2%; Score 53; DB 16; Length 378; Best Local Similarity 45.5%; Pred. No. 10+02; Matches 10; Conservative 3; Mismatches 9; Indels
                   Score 53; DB 17; Length 303;
Pred. No. 79;
                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_59285C.1.pep
US-10-437-963-159960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELATING TO HELICOBACTER
                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows NT 4.0
                                                                                                 12 CDLWINEMS-LLHKIVQD---VYGTPHPP 36
                                                                                                                         Sequence 159960, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 RSSFCCLWLNNCFSNHKIVQQI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 RGTECDLWINEMSLLHKIVQDV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                 Query Match
Best Local Similarity 37.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                          10-437-963-159960
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Gaps

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Length 468;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53 ; Search time 9.32076 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-46 210 1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTPHPPHS 38 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		æ			SOUTHER	
Result		Query				
No.	Score	Match	Length	BB	QI.	Description
	57	27.4	308	N	385	1 prot
7	57.5	27.4		N	T40213	ical
٣	57	27.1		~		Н
4	57	27.1	1116	7	_	덭
Ŋ	55		312	N	T20932	_
9	54	25.7	245	N	16	ra ra
7	54	25.7	245	N	N	
œ	53	25.2	522	N	B71978	_
o	52	24.8	131	N	AF3338	_
10	51.5	24.5	297	N	T08589	hypothetical prote
11	51	24.3	186	~	A81272	
12	51	24.3	259	N	A98302	oligopeptide trans
13	51	24.3	259	N	AG2981	hypothetical prote
14	0	24.0	181	N	G85930	racts wit
15	50.5	24.0	181	N	E91085	protein (i
16	О	24.0	181	~	A55944	protein
17	0	24.0	336	~	C86921	erved hypo
18	0	24.0	561	~	AE2649	alpha-glucosidase
19	0	24.0	594	~	D97431	probable alpha-glu
20	O	24.0	837	N	H84239	dimethylsulfoxide
21	20	23.8	190	Н	D64566	dCTP deaminase (EC
22	20	23.8	227	~	C84431	hypothetical prote
23	50	23.8	232	N	D71157	probable haloacid
24	20	23.8	300	~	T00274	hypothetical prote
25	20	23.8	361	N	H96634	ical
26	20	23.8	459	N	07	elle
27	50	23.8	483	N	753	hypothetical prote
28	20	23.8	579	~	185	a]
29	20	23.8	821	~	T16412	_

aspartate kinase (	ribosome recycling	hypothetical prote	hypothetical prote	acetylornithine de	aspartyl aminopept	transcription adap	transcription coac	CREB-binding prote	protein ZK632.10 [	oxidoreductase, Gf	conserved hypothet	hypothetical prote	serine O-acetyltra	Xdll-2 protein - c	probable regulator
T04752	AE1957	T16335	F72476	F83984	F96974	A54277	S39162	S39161	B88567	F95153	G87636	E70366	A84936	I51258	T35917
01	C4	<b>C</b> 4	~	N	N	N	(7)	N	N	N	N	N	N	N	N
916	182	223	283	427	433	2414	2440	2441	80	379	429	165	274	277	332
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23	23.3	23.3	23.3	23.3	23.3	23	23.3	23	23.1	23	23	22.9	22	22	22
0.0	49	49	49	49	49	49	49	4	48.5	48.5	48.5	48	48	48	48
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
hypothetical protein BH1668 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83856
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: D83858
A;Equers preliminary
A;Residues: 1-308 <ATO>
A;Accession: D8386s
A;Accession: Camplete Cype: DNA
A;Residues: L308 <ATO>
A;Cross-references: UNIPROT:09KCAS; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BABOS C;Genetics:
A;Gene: BH1668
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Cispecies: Schizosaccharomyces pombe
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibacesion: T40213
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Cibacesion: T40213
Cibacesion: Cibaces: UNIPROT: P87311; EMBL: Z87204; PIDN: CAB10087.1; GSPDB:GN00067; SPDB: SA; Experimental source: strain 972h-; cosmid c31F10
Cibacesion: SPDB: SPBC31F10.10c
Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: Cibacesion: 
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27.4%; Score 57.5; DB 2; Length 308;
Best Local Similarity 46.2%; Pred. No. 3.7;
Matches 12; Conservative 5; Mismatches 4; Indels
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27.4%; Score 57.5; DB 2; Length 574;
Best Local Similarity 41.2%; Pred. No. 7.3;
Matches 14; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 DLWVS-LCEAHRI----YGTTHPPNS 209
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A;Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                               A,Cross-references: UNIPROT:093482, EMBL:Z81061; PIDN:CAB02931.1, GSPDB:GN00023, CESP:F:
A,Experimental source: clone F14H8
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A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; cross references: UNIPROT:08U736; GB:AE008689; PIDN:AAL45414.1; PID:g17743114; GSPDB:
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:Q8U736; GB:AE007870; PIDN:AAK88827.1; PID:g15158585; GSPDB:
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C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan.-2002 #sequence_revision 11-Jan.-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Agrobacterium tumefaciens
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Préd. No. 8.2;
4; Mismatches 10;
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                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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25.7%; Score 54;
Best Local Similarity 40.0%; Pred. No. 4
Matches 12; Conservative 3; Mismatch
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A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.2%;
Best Local Similarity 40.5%;
Matches 15; Conservative
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A,Map position: linear chromosome
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A.Molecule type: DNA
A.Residues: 1-245 <KUR>
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A;Molecule type: DNA
A;Residues: 1-245 <KUR>
                                                                                                                                                                                                                                                                                                                          A; Map position: 5
A; Introns: 79/3; 136/3
                                                                                                                                                                                                                                                                                          A, Gene: CESP: F14H8.2
                               A; Accession: T20932
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Acession: B70476
A;Accession: B70476
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DNA
A;Residues: 1-1116 <AQP>
A;Cross-references: UNIPROT:O67838; GB:AE000770; NID:g2984274; PIDN:AAC07805.1; PID:g298
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                           hypothetical protein Rv3614c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70956
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
NAture: Becophering the biology of Mycobacerium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Accession: G70956
A;Accession: G70956
A;Accession: DAA
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3614c
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C;Date: 08-May-1198 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70476
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20932
S;Matthews, L.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pothetical protein ag 2054 - Aquifex aeolicus
Species: Aquifex aeolicus
Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 184;
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                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.1%; Score 57; DB 2
Best Local Similarity 35.3%; Pred. No. 2.4;
Matches 12; Conservative 7; Mismatches
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                                       3 MLLDRRGTECDLWINEMSLLHKIVQDVYGTPHPP
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Matches 13; Conserv
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"Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: A98302
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldmar A; Liu, F.; Wolllam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. A; Liu, F.; Wolllam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                 C;Accession: T06589
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16098
A;Accession: T08589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable dCTP deaminase (EC 3.5.4.13) Cj1292 [imported] - Campylobacter jejuni (strain C;Species Campylobacter jejuni (strain C;Species Campylobacter jejuni (c)Accession: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: A81272 Mren, W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Wnitehead, S.; Barre Nature 403, 665-668, 2000 A;Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:09PN07; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB737
A;Experimental source: serotype O2, strain NCTC 11168
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A;Molecule type: DNA
A;Residues: 1-259 <KUR>
A;Cross-references: UNIPROT:Q8UAB8; GB:AE007870; PIDN:AAK89939.1; PID:g15159894; GSPDB:
C;Genetics:
                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9SZZ0; EMBL:AL050398; GSPDB:GN00062; ATSP:L23H3.40
A;Experimental source: cultivar Columbia; BAC clone L23H3
C;Genetics:
A;Gene: ATSP:L23H3.40
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4
A;Introns: 9/3; 44/3; 82/3; 142/3; 169/2; 196/2; 225/3; 252/3
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Pred. No. 16;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
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GLKADNWIRKMALEHKMIE 20
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Best Local Similarity 54.2%;
Matches 13; Conservative
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A/Gene: dcd, Cj1292
C'Superfamily: dCTP deaminase
C'Keywords: hydrolase
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-297 <BEV>
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A;Molecule type: DNA
A;Residues: 1-186 <PAR>
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-131 <kUR>
A;Cross-references: UNIRROT:08YHV4; GB:AE008917; PIDN:AAL51873.1; PID:g17982624; GSPDB:GCGenetics: BxEndels
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Helicobacter pylori
A;Variety: strain J99
Date: 19.004
C;Date: 19.004
C;Date: 19.009
C;Accession: B71979
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT.09ZN06; GB:AE001445; GB:AE001439; NID:g4154559; PIDN:AAD0563
A,Experimental source: strain J99
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                  Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein jhp0054 - Helicobacter pylori (strain J99)
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                                                                                                      Indels
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T08589
hypothetical protein L23H3.40 - Arabidopsis thaliana
                                  DB 2;
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34.8%; Pred. No. e;
...a 5; Mismatches
                                                                                                   3; Mismatches
                                                                                                                                                                                                                     | | | : | | | | RGRE-----ELKLAQMVFQDPYGSLHPRH 96
                                                                                                                                                                           8 RGTECDLWINEMSLLHKIVQDVYGTPHPPH 37
                                  Score 54;
Pred. No.
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                          Query Match
Best Local Similarity 40.0%;
Matches 12; Conservative
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Best Local Similarity 34.8
Matches 8; Conservative
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A;Gene: jhp0054
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B9-Jul-2001
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Rteference number: A99629; MUD:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA.
A,Residues: 1-181 -HAX>
A;Cross-references: UNIRROT:Q8X6T2; GB:BA000007; PIDN:BAB37076.1; PID:g13363125; GSPDB:
A,Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                               Syd protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
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C,Superfamily: Escherichia coli syd protein
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Best Local Similarity 34.2%;
Matches 13; Conservative '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu3456 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG581
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Levy, R.; Li, M.; McClell
Frarp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Atuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-259 -KUR>
A; Residues: 1-259 -KUR>
A; Cross-references: UNIPROT:Q8UAB8; GB:AE008689; PIDN:AAL44269.1; PID:g17741855; GSPDB:G
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Gene: Atu3456
A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-181 <STO>
A,Cross-references: UNIPROT:Q8X6T2; GB:AE005174; NID:g12517269; PIDN:AAG57907.1; GSPDB:G
A,Experimental source: strain O157:H7, substrain EDL933
C;Genetias:
A,Gene: syd
C;Superfamily: Escherichia coli syd protein
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: GBS930
R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A885480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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24.0%; Score 50.5; DB 2; Length 181;
Best Local Similarity 34.2%; Pred. No. 19;
Matches 13; Conservative 4; Mismatches 14; Indels 7
                                                                                                    Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51, DB 2; Length 259,
Pred. No. 24;
5; Mismatches 19; Indels
                                                                                                Query Match
24.3%; Score 51; DB 2; Length 259
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 5; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AQALKDFTARYCDAWHEE----HKSWPLSEELYGVPSP 39
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A;Gene: AGR L_2744
A;Map position: linear chromosome
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Best Local Similarity 33.3%;
Matches 12; Conservative
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A, Status: preliminary .
A, Molecule type: DNA
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3

Gaps

7 ;

Score 50.5; DB 2; Length 181; Pred. No. 19; 4; Mismatches 14; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:38:57; Search time 50.6189 Seconds (without alignments) 431.938 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-092-750-46 210 1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTPHPPHS 38

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q6c6t9 yarrowia li	Q93q79 rhodococcus	Q6sgv8 uncultured	Aas07882 unculture				O06269 mycobacteri			Q8i7z3 plasmodium	Q961b9 drosophila	O67838 aquifex aeo	Q8i332 plasmodium			Q93482 caenorhabdi	Q9k4e9 streptomyce		Q7m762 mus musculu	Q9gqc3 brugia mala			ıo	~	. streptomy	m	_	_	298 homc	
SUMMARIES		ID	Q6C6T9	093079	Q6SGV8	AAS07882	Q82N43	Q9KCA5	YB2A_SCHPO	006269	Q7TW35	Q81527	Q817Z3	Q961B9	YK54 AQUAE	Q813 <u>3</u> 2	Q810Z0	ARGD_BIFLO	Q93482	Q9K4E9	Q9CYU9	Q7M762	£20560	Q9FW76	Q7CVF0	080736	DXR_BUCAP	Q9RLS1	Q99YK8	Q8NZY7	CV04 HUMAN	CAG30298	Q8N7D6
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	Query	Match	31.9		27.6	27.6	27.6	27.4	27.4		27.1	27.1	27.1	27.1	27.1		26.9								25.7				25.7		25.7	25.7	25.7
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Q8a3p3 bacteroides	Q96pw0 homo sapien	Q8nf68 homo sapien	Q96je7 homo sapien	Q7s2q7 neurospora	Q8iqn5 drosophila	Aanl1756 drosophil	Q7r656 giardia lam	Q8ibw7 plasmodium	Q8i220 plasmodium	Q8pmb4 xanthomonas	Q6qvt6 micromonosp	Aar98555 micromono	Q81186 oryza sativ
Q8A3P3	O96PW0	Q8NF68	Q96JE7	078207	QBIQNS	AAN11756	Q7R656	Q8IBW7	Q81220	Q8PMB4	QGQVT6	AAR98555	Q8LL86
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655	757	789	1060	281	693	693	1230	2192	2646	103	268	268	378
25.7	25.7	25.7	25.7	25.5	25.5	25.5	25.5	25.5	25.5	25.2	25.2	25.2	25.2
54	54	54	54	53.5	53.5	53.5	53.5	53.5	53.5	23	23	23	53

# ALIGNMENTS

1	Q6C6T9 PRELIMINARY; PRT; 634 AA. O6C6T9;	(TrEMBLrel. 28, Creat	(TrEMBLrel. 28, Last	(TremBirel, 28, Last	Caromosome E of Strain CLIB99 of Yarrowia libolytica.	UKFNAMES=IALIJUEO836999;	Varrowia libolytica (candida libolytica).	bunatyola; raugul; Ascollatolliyoloa; saccilatolliyoloa; Sacohartootalaa: Dirocharcadaaa Vartolliyooliia; saccilatolliyoeles;	NOTE BASTA OF STREET OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET	1.15 1.0XID=4.956.	ון ן מוקום מוקופות איז זי	OBCOENCE FACE N.A.	GENOTERURES	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,	Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,	Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	Hancraye F., Henneduin C., Jauniaux N., Joyet P., Kachouri K.,	Kerrest A., Koszul K., Lemaire M., Lesur I., Ma L., Muller H., Misser A., Misser H.,	Micada U.M., Mindiski M., Ozcas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,	Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,	Α.,	,		"Genome evolution in yeasts.";	Mature 430:35-44(2004).	W MOGE CONSTITUTE	STRAIN-CLIEBS:	Genoscope;	Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.	382131; CAG79204.1;	SEQUENCE 634 AA; 68768 MW; 141B56A27228602F CRC64;	Query Match Best Local Similarity 37.1%; Pred. No. 1.9; Matches 13; Conservative 7; Mismatches 5; Indels 10; Gaps	3 MILDRRGTECDIWINEMSLIHKIVQDVYGTPHPPH 37		161 VIMDRRGQITHVYNQEVYGTPNPPN 185
RESULT Q6C6T9	e S	DŢ	E E	i i	2 5	2 0	2 C	35	3 8	5 6	Z 6	א ני ה	2 2 2	Z.	RA	RA	RA	R.	S S	\$ 8	<b>\$</b> 6	£ \$	RA	R.	R.	8 E	¥ 5	7 2	2 0	RC P	Z.	꿃	DR	ÖS	On Be Ma	ò	i	2

RESULT 2 Q93Q79 ID Q93Q79 AC Q93Q79;

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167 AA. PRT; PRELIMINARY; 537 AA.

PRT;

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Query Match
Best Local Similarity 45.8
Matches 11; Conservative
PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                      Haddad S., Eby D.M., Naidle E.L.;
Haddad S., Eby D.M., Naidle E.L.;
Haddad S., Eby D.M., Naidle E.L.;
"Cloning and expression of the benzoate dioxygenase genes from Rhodococus sp. strain 19070.";
Appl. Environ. Microbiol. 67:2507-2514 (2001).

BMBL; AF279141; AAK58904.1;
GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0016702; F:catalytic activity; IEA.

GO; GO:0016702; P:aromatic compound metabolism; IEA.

InterPro; IPR000391; Ring hydroxyl B.

Pfam; PF00866; Ring hydroxyl B.
                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Nocardiaceae, Rhodococcus.
NCBI_TaxID=161384;
                                                                                                                                                                                                                                                                                                                                                        29.3%; Score 61.5; DB 2; Length 167; 38.6%; Pred No. 2.4;
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Pred. No. 29;
3; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1
SEQUENCE FROM N.A.
Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AV458641; AS0078921; ---
InterPro: IFR001005; Myb DNA binding.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
Hypothetical protein.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeLong E.F.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  167 AA; 19861 MW; CAD4ECD83D692D91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Benzoate dioxygenase small subunit.
                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                               MEDLINE=21268842; PubMed=11375157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                environmental samples.
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05-JUL-2004 (TrEMBLrel. 27, Le
05-JUL-2004 (TrEMBLrel. 27, Le
Hypothetical protein.
ORFNames=EBACO80-L32B05.10;
uncultured bacterium 463.
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Best Local Similarity 45.89
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 38.6
Matches 17; Conservative
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                                                                    Rhodococcus sp. 19070.
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STRAIN=MA-4680;
MEDLINE=2508306; PubMed=12692562;
MEDLINE=2508306; PubMed=12692562;
Sakaki Y., Hattori M., Omura S.;
Sakaki Y., Hattori M., Omura S.;
Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL, ABOGSO7; BAC63170.1;
InterPro; IPR004941; TPR-1ixe.
Pfam: PR00515; TPR; 4.
PROSITE: PS05293; TPR; 4.
PROSITE: PS05293; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                           DeLong B.F.;
"Monterey Bay Coastal Ocean Microbial Observatory environmental clone
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 26, Last annotation update)
Putative ATP/GTP-binding protein.
OrderedLocusNames=SAV1460;
Streptomyces avermitilis.
Streptomyces Streptomycetales; Streptomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.6%; Score 58; DB 2; Length 537; 45.8%; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong B.F.; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AY458641; AAS07882.1; ... Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 protein.
537 AA; 58971 MW; 443FCC7B86231264 CRC64;
                                                                                      Last annotation update)
                                                     Last sequence update)
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            Created)
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MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                 uncultured bacterium 463.
Bacteria, environmental samples.
NCBI_TaxID=257394;
...EMBLrel. 27, Cl
02-MAR-2004 (TrEMBLrel. 27, La
02-MAR-2004 (TrEMBLrel. 27, La
Hypothetical protein.
EBACO80-L32805.10.
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Mycobacterium tuberculosis.
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EMBL, APO01512; BAB05387.1; -...
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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                                            DB 2; Length 1011; 60;
SEQUENCE 1011 AA; 111014 MW; 2ADBEA2562166AA9 CRC64;
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SEQUENCE 308 AA; 35202 MW; 39DB871087B7DE77 CRC64;
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Last annotation update)
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P87311,
16-0CT-2001 (Rel. 40, Last sequence update)
05-UJU-2004 (Rel. 44, Last annotation update)
Hypothetical protein C31F10.10c in chromosome II.
ORYMANES-SPBC31F10.10c;
                                                                                                                                                                                              1 AAMLLDRRGTECDLWINEMSLLHKIVQDVYGTPHP 35
                                                    ch 27.6%; Score 58; DB:
1 Similarity 37.1%; Pred. No. 60;
13; Conservative 8; Mismatches
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46.2%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
BH1668 protein.
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les 12; Conservative
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                                              Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                         Matches
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RESULT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Chiver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutter S., Saunders D., Seeger K., Sharp S., Sketon U. Simmonds M., Squares F., Squares S., Stevens K., Taylor K.G., Tivey A., Walsh S.V., Warren T., Whitchead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wolfaert G., Pritzc C., Helzer E., Moestl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S., Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure K., Hurst S.M., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Poteshkin J., Rhe genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe.";

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Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
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PROSITE; PS01560; ZF_MYND 1; 1.
PROSITE; PS0665; ZF_MYND 2; 1.
DNA-binding; Hypothetical protein; Nuclear protein; Zinc-finger.
ZN_FING
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64142 MW; E66B8B23164D5F75 CRC64;
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MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein MT3716.
OrderedLoousNames=MT3716, Rv3614c;
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41.2%; Pred. No. 37;
ive 6; Mismatches 11;
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PIK; T40213; T40213.
GeneDB SPombe; SPBC31F10.10c; -.
InterPro; IPR008938; ARM.
InterPro; IPR002893; Znf_MXND.
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MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Petrea M., Allan J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Erauhholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carlocol D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel, 23, Created)
01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
4-methyl-2-beta-hydroxyethylthiazole kinase.
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida, Plasmodium.
NCBI_TAXID-5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Tami G., Pelle R., Mulaa F.J.; Submid. G., Pelle R., Mulaa F.J.; Submid. G., Pelle R., Mulaa F.J.; Submid. Mulad. (CCT-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY166865; AAN86918.1; -.. Marsp.; PS9591; LEXG. GO: 00004417; F: Hydroxyethylthiazole kinase activity; IEA. GO; GO:0009228; P: thiamin biosynthesis; IEA. FixerProx. TRG00417; Hyethyz_kinase. FP02110; HK; 1. PRITZKNASE.
                                                                                                                                             Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: GO:0004417; F.hydroxyethylthiazole kinase activity; IEA.
GO: GO:0009228; P:thiamin biosynthesis; IEA.
InterPro: IPR000417; Hyethyz_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyman R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda Nakao B., Rowley D., Tamaki T., Wang F., Davis R.W.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AE014850; AAN36470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 2; Length 302;
Pred. No. 20;
2; Mismatches 6; Indels
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                                                01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
Hydroxyethylthiazole kinase, putative.
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302 AA.
                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01099; HYETHTZKNASE.
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                           (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   falciparum.";
Nature 419:498-511(2002).
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                                              01-MAR-2003
01-MAR-2003
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SEQUENCE
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Q817Z3
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                                                                                                                                                         STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Managor T., Bigineler K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

BMBL; BX248346; CAD95830.1; -
COMPLete proteome; Hypothetical protein.

SEQUENCE 184 AA; 19834 MW, 6326911F65DC5C7A CRC64;
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Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deckphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544 [1998).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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27.1%; Score 57; DB 2; Length 184; Best Local Similarity 35.3%; Pred. No. 12; Matches 12; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.1%; Score 57; DB 2; Length 184; Best Local Similarity 35.3%; Pred. No. 12; Matches 12; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist; Rv3614c; -. Complete protein. Complete proteome; Hypothetical protein. SEQUENCE 184 AA; 19834 MW; 6326911F65DC5C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Mb3644c.
OrderedLocusNames=Mb3644c;
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MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
BmbL; BX842583; CAB08952.1; -.
EMBL; AE007171; AAK48075.1; -.
PIR; G70956; G70956.
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                                                                                                                                             SEQUENCE FROM N.A.
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Q7TW35; Q7TW35

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RESULT 10 Q81527

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Science 287:2185-2195(2000).
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Matches
 8
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RA Adams MD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams MD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams MD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams MD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Gucroe R.A., Lewis S.E., Richards S., Ashburner M., Hedderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutton G.G., Wortman J.R., Blazej R.G., Champen M., Pfeiffer B.D.,

RA Ballew R.M., Baru A.M. Baxendale J., Bayraktarologu L., Beasley E.M.,

Ballew R.M., Baru A.M., Baxendale J., Bayraktarologu L., Beasley E.M.,

RA Beeson K.Y., Bencos P.V., Burler H., Buck G., Bhandari D., Blothakov S.,

RA Burtis K.C., Busem D.A., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busem D.A., Dahlke C., Perraz C., Ferriar C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Gargins C., Dowler B., Davies P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L.,

RA Hostin D., Houston K.A., Heiman T.J., Harrier S., Lin X.,

RA Hostin D., Houston K.A., Heiman T.J., Harris M.D., Rechum K.A.,

RA Hostin D., Harryey D., Heiman T.J., Wei M.H., Ibeywam C.,

Alaluh M., Kalush F., Karpen G.H., Ke Z., Keminson J.A., Ketchum K.A.,

RA Hostin D., Houston K.A., Moy M., Murphy S., Moshrefi A.,

Mount S.M., Moy M., Murphy S., Murphy L., Murshy D.M., Nelson D.L.,

RA Mennel B.E., Kedira C.D., Karate C., Kravitz S., Kulp D., Lai Z.,

RA Balazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Shue B.C., Siden-Kiamos I. Singson M., Strong R., Such B.,

RA Shrakasarman D.A., Weinstock G.M., Weissenbach J., Wang X.,

Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Waller H., Sander M., Shiber E., Shadelland S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaveri J.S., Zaver
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Ninco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
               Length 302;
                                           6; Indels
                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
              5
              Score 57; DB
Pred. No. 20;
                                          Mismatches
                                                                                    272 SLSHKIIDDIYYYSHNPH 289
                                                                      SLLHKIVQDVYGTPHPPH 37
            27.1%;
55.6%;
                                                                                                                                                                                    Q961B9; Q9VUZ7;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
05-JUL-2004 (TrEMBLrel. 27,
                                        10; Conservative
                                                                                                                                                                         PRELIMINARY;
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ORFNames=CG5027;
          Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
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Q961B9
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Calsequestrin is a high-capacity, moderate affinity, calcium-binding protein and thus acts as an internal calcium store in muscle. The release of calcium bound to calsequestrin through a calcium release channel triggers muscle contraction (By similarity).
MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster enchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 430;
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Calcium, Calcium-binding; Redox-active center.
SEQUENCE 430 AA; 49507 MW; 782F66BF5607DFF7 CRC64;
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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50.0%; Pred. No. 31;
cive 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR001393; Calsequestrin.
InterPro, IPR006662; Thiored.
InterPro, IPR006663; Thioredox_dom2.
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PRINTS; PR00312; CALSEQUESTRN.
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomics perspective.";
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es 10; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified on-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2255708; PubMed=12368867; Harris B., Harris D., Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Hall N., Bowman S., Arkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Croinin A., Davies R., Davis R., Dearden F., Doggett J., Crolnin A., Goble A., Goodhead I., Gwilliam R., Hamin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                        MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PFI0585c.
Name-PPI05885c;
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1116; 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1; Length 111
Pred. No. 93;
6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1116 AA; 127794 MW; 423E5FCC6C02C89C CRC64;
                                                                                                                                                                                                                           Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Hypothetical protein; Transmembrane.
                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Hypochetical protein AQ 2054.
OrderedLocusNames=AQ_2054;
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                                                                                        1116 AA
                                                                                        PRT;
301 WIGEPSIAHSIILDQLPTPH 320
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InterPro; IPR007452; DUF490.
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Best Local Similarity 41.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
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                                                                                        STANDARD;
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Q81332
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MEDLINE=22507960; PubMed=12620990;
MEDLINE=22507960; Staletsky H., Akutsu H., Berry D.L.,
Vanagimachi R., Page D.C., Jaenisch R.;
"Incomplete reactivation of Oct4-related genes in mouse embryos cloned
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., McLean J., Mooney P., Woule S., Murphy L., Oliver K., Ormond D., Prico, C., Quail M.A., Rabbinowitsch E., Sajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin L., Whithead S., Woodward J., Sulston J.E., Craig A., Mebbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; Mature 419:527-531(2002).

EMBL; AL929356; CADS1803.1; -.

Hypotherical protein.

SEQUENCE 1568 AA; 188685 MW; FID966E66CB78DE7 CRC64;
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Frame14;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                     4;
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Local Similarity 39.4%; Pred. No. 44;
local 13; Conservative 4; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                Length 1568;
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Last annotation update)
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27.1%; Score 57; DB 2; L
Best Local Similarity 48.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from somatic nuclei.";
Development 130:1673-1680(2003).
EMBL; AP490140; AAO84498.1; -.
MGD; MGI:2156377; Pramel4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Q810Z0;
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us-10-092-750-47.rai

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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Query Match
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Sequence 19052, A
Sequence 19545, A
Sequence 4254, Ap
Sequence 288, App
Sequence 22673, A
Sequence 22673, A
Sequence 22673, A
Sequence 22599, A
Sequence 22589, A
Sequence 22589, A
Sequence 22, Appl
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-19052
US-09-621-976-4254
US-09-621-976-4254
US-09-621-976-4254
US-09-252-991A-18764
US-09-252-991A-28585
US-09-252-991A-28585
US-09-252-991A-28585
US-09-562-737-29
US-09-562-737-29
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US-09-562-737-29
US-09-296-715-4
US-09-296-715-4
US-09-296-715-4
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US-09-252-991A-27971
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US-09-252-991A-19257
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Maximum Match 100%
Listing first 45 summaries
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124
1 PWQYKPIADLYRGRESRPSAPR 22
                                                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                                                                                                    OM protein -
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Sequence 2400, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
TTPLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 7709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2400

LENGTH: 293
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                                          Sequence 2578, App Sequence 138, App Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 14, Appl Sequence 14, Appl Sequence 2731, Appl Sequence 2558, Appl Sequence 2558, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl Sequence 5058, Appl
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Sequence 7218, Ap
Sequence 19118, A
Sequence 5, Appli
Sequence 6, Appli
Sequence 2007071
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44.4%; Pred. No. 9.8;
tive 3; Mismatches 7; Indels
US-09-252-991A-20678

US-09-540-256-2578

US-08-795-868-16

US-09-303-069-16

US-09-303-069-16

US-09-303-069-14

US-09-303-069-14

US-09-303-069-14

US-09-303-069-14

US-09-328-352-503

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Sequence 19052 Application US/09252991A

Fateri No. 655195

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEON

TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEON

TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEON

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity 44.4
Matches 8; Conservative
            TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2400
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Length 650;

DB 4;

Score 48;

38.7%;

US-09-252-991A-18764

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Sequence 18764, Application US/0925291A

Sequence 18764, Application US/0925291A

Sequence 18764, Application US/0925291A

Sequence 18764, Application US/0925291A

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILER REPRENCE: 107196.18

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18764

LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33304NCE: P3140,1002
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 4; Length 297;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 548 LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 548, Application US/10140002 Patent No. 6725730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 PWESKNSTAVWRGRDSR 313
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative ;
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapien
US-10-140-002-548
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-18764
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// Sequence 19645, Application US/09252991A
// Sequence 19645, Application US/09252991A
// Patent No. 655195
// GENERAL INFORMATION:
// APPLICATION:
// APPLICATION:
// APPLICATION:
// APPLICATION NUMBER:
// CURRENT FILING DATE: 1999-02-18
// PRIOR PAPLICATION NUMBER: US 60/074,788
// PRIOR PAPLICATION NUMBER: US 60/074,190
// PRIOR PILING DATE: 1998-07-27
// NUMBER OF SEQ ID NOS: 33142
// SEQ ID NO 19645
// LENGTH 881
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Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.7%; Score 48; DB 4; Length 851; Best Local Similarity 40.9%; Pred. No. 61; Matches 9; Conservative 4; Mismatches 7; Indels
                        Indels
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; Patent No. 6639063;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Undert, S.
APPLICANT: JODERT, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
LENGTH: 151
                          4;
    66.7%; Pred. No. 46; ive 1; Mismatches
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; OTHER INFORMATION: Xaa = Phe, lle, Leu, Val
VS-09-621-976-4254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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84 PWESKNSTAVWRGRDSR 100
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                                                                                                              436 ADLGRGPRSRPARPR 450
                                                                 8 ADLYRGRESRPSAPR 22
    Best Local Similarity 66.7
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-19645
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RESULT 5

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GENERAL INFORMATION:
APPLICANT: MACC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 458
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US-09-562-737-22
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                                                                                                                                                                                                                                                                                       Length 372;
                                                                                                                                                                                                                                                                                                                                       8; Indels
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US-09-562-737-22

Sequence 22, Application US/09562737
Parent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz. Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPRENCE: UTSW0708
CURRENT APPLICATION UNDER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 724
                                                                                                                                                                                                                                                                                       Score 46; DB 4;
Pred. No. 50;
5; Mismatches
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 372
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US-092-252-991A-28585
; Sequence 28585, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                   1 PWQYKPIADLYRGRESRPSAPR 22
                                                                                                                                                                                                                                                                                                                                                                                                                      61 PCRWRPNAGTGRARPTAPAAPR 82
                                                                                                                                                                                                                  , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
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Sequence 32954, Application US/09252991A

Sequence 32954, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196, 136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NO 32954

LENGTH: 285

LENGTH: 285
                                                     Sequence 22673, Application US/09252991A

Sequence 22673, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Maxc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22673

LIENGTH: 186
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37.1%; Score 46; DB 4; Length 186;
Best Local Similarity 52.9%; Pred. No. 24;
Matches 9; Conservative 1; Mismatches 7; Indels
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37.1%; Score 46; DB
Best Local Similarity 58.8%; Pred. No. 38;
Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32954
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                                                  US-09-252-991A-22673
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US-09-513-999C-7998
US-09-513-999C-7998
Sequence 7998, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATEL REPERBNOE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER: OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7998
LEMOTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 204;
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APPLICANT: O'SEBER, DANIEL
APPLICANT: O'SEBER, DANIEL
TILLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: BOXYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: BOXYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: BOXYBEAN
CORRESSED: 32
CORRESSED: B.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATE: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
36.7%; Score 45.5; L
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches
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; Sequence 4, Application US/08924747
; Patent No. 6063570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY JAGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: CL-1:
TELECOMMUNICATION INFORMATION:
TELECHONE: 302-892-8112
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acid
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ORGANISM: Homo sapiens
US-09-513-999C-7998
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Patent No. 6783961

GENERAL INFORMATION

APPLICANT: Dunclert, A.

APPLICANT: Dunclert, A.

APPLICANT: Dunclert, A.

APPLICANT: Giordano, J.Y.

APPLICANT: Giordano, J.Y.

TILE REPERENCE: 59. US. REG

FILE REPERENCE: 59. US. REG

CURRENT FILING DATE: 2000-02-24

PRIOR PILICATION NUMBER: US 60/122, 487

PRIOR PILICATION NUMBER: US 60/122, 487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 7997

LENGTH: 204

TYPE: PRI CONCLEMENT: Ratent.pm

SEQ ID NO 7997

LENGTH: SAME CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLEMENT: CONCLE
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                                                   Query Match 37.1%; Score 46; DB 4; Length 724; Best Local Similarity 42.9%; Pred. No. 1e+02; Matches 9; Conservative 2; Mismatches 10; Indels
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37.1%; Score 46; DB 4; Length 724;
Best Local Similarity 40.9%; Pred. No. 1e+02;
Matches 9; Conservative 3; Mismatches 10; Indels
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Sequence 29, Application US/09562737

Patent No. 642867

GENERAL INFORMATION:

APPLICANT: Herz, Joachim

APPLICANT: Gotthardt, Michael

TITLE OP INVENTION: LDL Receptor Signaling Pathways

FILE REFERENCE: UTSW0708
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36.7%; Score 45.5; D
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches
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CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 PRRYSPVASDLLGEEDIPTEPR 312
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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1 PWQYKPIADLYRGRESRPSAPR
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Perfect score:
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                                                                                                                                                    Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

### Sequence 47, Appl Sequence 13264, A Sequence 11116, Sequence 11116, Sequence 15960, A Sequence 15960, A Sequence 1584, A Sequence 1584, A Sequence 3278, A Sequence 371, Appl 15960, A 16323, A 15584, A 3278, Ap 71, Appl 70, Appl 274406, 3026, Ap Description Sequence Sequence Sequence US-10-092-750-47 US-10-425-115-333161 US-10-425-115-333161 US-10-417-700A-7 US-10-369-493-11516 US-10-369-493-15323 US-10-369-493-15584 US-10-094-749-358 US-10-120-801-70 US-10-120-801-70 US-10-120-801-70 US-10-120-801-70 Query Match Length DB Score 1111 12110987654321 8

RESULT 2
US-10-425-115-333161
; Sequence 333161, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

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APPLICANT: Barbazuk, Brad Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Li, Pari Applicant: Richard Applicant: Reference: 38-21(3321)B CURRENCE: 38-21(33221)B CURRENCE: 38-21(33221)B CURRENCE: 2003-05-14 Applicant: NUMBER: US/10/437,963 CURRENCE: SEQ ID NO: 204966 SEQ ID NO: 111116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinke, 'Gregory J.
APPLICANT: Hinke, 'Gregory J.
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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US-10-437-963-111116
                                                                                                                                                                                                                                                                                           Score 50; DB 15;
Pred. No. 1e+02;
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Pred. No. 47;
4; Mismatches 9
       TITLE OF INVENTION: peptide synthetase systems
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                         FILE REFERENCE: 3002-140S
CURRENT APPLICATION NUMBER: US/10/417,700A
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 139
SOFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111116, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15960, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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410 PVADVRPGRVSRPAAGR 426
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                            6 PIADLYRGRESRPSAPR 22
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Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local Similarity 40.9%;
Matches 9; Conservative
                                                                                                                                                                                               TYPE: PRT ORGANISM: Actinoplanes sp.
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ORGANISM: Oryza sativa
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NAME/KEY: unsure
LOCATION: (1)..(1
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                                                                                                                                                                             LENGTH: 445
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Sequence 7, Application US/10417700A
Publication No. US20040033581A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFPA, Alfredo
APPLICANT: FARRET, Chris
IITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosom
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Town, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 333161
LENGTH: 61
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US-10-425-115-333161
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Pred. No. 2.8;
3; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION OWURA, SATOSHI
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: ISHIKAWA, UNN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TILLE ON INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13264, Application US/10156761
Publication No. US20030119018A1
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US-10-156-761-13264
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
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167 AELYGGRDNSPSAP 180
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SEQ ID NO 13264
LENGTH: 441
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Best Local Similarity
Then 9; Conserva
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US-10-417-700A-7
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Pred. No. 1.70+02;
1; Mismatches 5; Indels
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Pred. No. 1.7e+02;
6; Mismatches 6; Indels
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APPLICANT: NAGAHARI, KENII
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NUVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SCOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3278
LENGTH: 560
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 71, Application US/10120801; Publication No. US20030203843A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 YERKPLSSVYRPRLSKPEEP 38
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APPLICANT: Guo, Xiaojia
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly
                            TYPE: PRT
, ORGANISM: Xanthomonas campestris
US-10-369-493-15584
                                                                                                                                                                                                                                                    439 OPALDPYRGRÉISPSA 454
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Best Local Similarity 62.5%;
Matches 10; Conservative
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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OTSUKA, MOTOYUKI
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ISONO, YUUKO
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Best Local Similarity 40.03
Matches 8; Conservative
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SATO, HIROYUKI
ISHII, SHIZUKO
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IRIE, RYOTARO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-10-094-749-3278
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US-10-120-801-71
         LENGTH: 555
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Sequence 15584, Application US/10369493

Publication No. US20030233675A1

Publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

FILE REFERENCE: 38-10(5205)B

CURRENT FAILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SECOND IN NOS: 47374

SEQ ID NO 15584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16323, Application US/10369493

Sequence 16323, Application US/10369493

Publication No. US20000233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Gladman, Barry

APPLICANT: Gladman, Barry

APPLICANT: Gladman, Barry

APPLICANT: Gladman, Barry

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 16323
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                                                                                                                                                                                                                                                                       Query Match
39.5%; Score 49; DB 14; Length 552;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 10; Conservative 1; Mismatches 5; Indels
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15660
LENGTH: 552
                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                          436 OPALDPYRGREISPSA 451
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Sequence 3026, Application US/10320797
Sequence 3026, Application US/10320797
Sequence 3026, Application No. US20040014955A1
GENERAL INFORMATION:
APPLICANT: Erroshkin, Alexey M.
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND TITLE OF INVENTION: METHODS OF USE
FILE REPERENCE: 10182-021-99
CURRENT FILEM DATE: 2002-12-16
PRICR APPLICATION NUMBER: US/10/320,797
CURRENT FILEM DATE: 2001-12-16
PRICR FILING DATE: 2001-12-17
NUMBER: OF SEQ ID NOS: 3361
SEQ ID NO 3026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 274466, Application US/10425115
Sequence 274466, Application US/10425115
Sequence 274466, Application No. US20040214272A1
Sequence 274466, Application No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: APPLICANT: Chou, Yihua
APPLICANT: Chou, Youla
APPLICANT: Chou, Youla
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 274466
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 14; Length 1163;
Pred. No. 3.66+02;
4; Mismatches 8; Indela C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.7%; Score 48; DB 17; Length 84; Best Local Similarity 50.0%; Pred. No. 37; Matches 11; Conservative 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
3. OTHER INFORMATION: Clone ID: MRT4577_181849C.l.pep
0S-10-425-115-274406
                  PRIOR APPLICATION NUMBER: 60/291241
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 70
LENGTH: 1163
TYPE: PRT
CREAMING: human
US-10-120-801-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1135 PIKLSPTSPVYRGSSSGPSSP 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PWQYKPIADLYRGRESRPSAP 21
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Similarity 42.9%;
9; Conservative '
FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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                  APPLICANT: Melifadail, Fuad.
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Walyankar, Uriel
APPLICANT: Wasserman, Scott
APPLICANT: Saithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Comtuber, Erik
APPLICANT: Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-340
FILE REFERENCE: 21402-340
FILE REFERENCE: 2002-04-11
FILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 2002-04-11
FILE OF INVENTION NUMBER: 60/28608
FILE REFERENCE: 2001-04-24
FRIOR PELING DATE: 2001-04-24
FRIOR APPLICATION NUMBER: 60/286292
FRIOR PELING DATE: 2001-04-25
FRIOR PELING DATE: 2001-04-25
FRIOR PELING DATE: 2001-05-16
FRIOR PELING DATE: 2001-05-16
FRIOR PELING DATE: 2001-05-16
FRIOR PELING DATE: 2001-05-14
FRIOR PELING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-04-20
NUMBER OF SOG ID NOS: 155
SOFTWARE PELING VALUE ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MASSELMENT, SALOUL
APPLICANT: Edinger, Shlomit
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Birk
APPLICANT: Gunther, Birk
APPLICANT: Gunther, Birk
APPLICANT: Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-340
CURRENT APPLICATION NUMBER: 60/285748
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/286068
PRIOR PILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/28629
PRIOR APPLICATION NUMBER: 60/286292
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/286393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.5%; Score 49; DB 14; Length 901; Best Local Similarity 42.9%; Pred. No. 2.8e+02; Matches 9; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Application US/10120801
Publication No. US20030203843A1
GENERAL INFORMATION:
APPLICANT: Pena, Carol
APPLICANT: Guo, xiaojia
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Schuda, Muralidhara
APPLICANT: Schuda, Kamesh
APPLICANT: Scytek, Kimberly
APPLICANT: Mehraban, Fuad
APPLICANT: Mehraban, Fuad
APPLICANT: Masserman, Scott
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873 PIKLSPTSPVYRGSSSGPSSP 893
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US-10-120-801-71
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Gaps

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Query Match 37.9%; Score 47; DB 16; Length 125; Best Local Similarity 47.6%; Pred. No. 76; Matches 10; Conservative 2; Mismatches 9; Indels
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US-10-437-963-187550
                                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(125)
UTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 11, 2004, 02:43:03 Job time : 26.4953 secs
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                      ORGANISM: Oryza sativa
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; Publication No. US200401233431
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Thou, Yihua
; APPLICANT: Thou, Yihua
; APPLICANT: Hou, Wei
; APPLICANT: Mu, Wei
; APPLICANT: Mu, Wei
; APPLICANT: Mu, Wei
; APPLICANT: Mu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: 11, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/437,963
; CURRENT PAPLICATION NUMBER: US/10/437,963
; UNWBER OF SEQ ID NOS: 204966
; SEQ ID NO 187550
; TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3763, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Stater, Steven C.

APPLICANT: Gladen, Rarry S.

APPLICANT: Gladen, Rarry S.

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                                                                                                                                                                                                               Score 48; DB 15; Length 212;
Pred. No. 92;
5; Mismatches 4; Indels
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; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-3763
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3026
                                                                                                                                                                                                                                                                                                                                                                                                                                        28 WEYRQLAVIHRA--SRPSRP 45
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                                                                                                                                                                                                               Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
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ORGANISM: Neurospora crassa
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53 ; Search time 5.39623 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

22 124 1 PWQYKPIADLYRGRESRPSAPR US-10-092-750-47 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		ij	hypothetical prote		11	proline dehydrogen	squamosa promoter	hypothetical prote	transcription regu	probable transcrip	probable phosphogi		glucosidase BH0704	ribosomal protein	conserved hypothet	SLN1 protein - yea	hypothetical prote	[47 pro	alpha-soluble NSF	alpha SNAP - human	alpa-SNAP protein	Ñ	choline dehydrogen	hypothetical prote	probable glucosyl	ECF family sigma f	ecf sigma factor (	hypothetical prote
SUMMARIES	ΙD	F72665	S74629	A84806	A85076	\$26380	T16141	T31343	T52297	E70633	AH2650	G97432	3	H84516	H83737	S	H72417	848387	859772	S16869	S58285	G02238	832367	S32368	***	61	35	AE2759	754	믑
	DB	. 7						~	~	7	7	~	7	7	N	-	7	Ņ	7	~	~	N	~	~	7	7	N	N	N	(1)
	° Query Match Length	187	488	217	282	204	432	1016	323	213	290	290	632	619	801	204	306	1220	208	247	295	295	295	298	567	574	869	168	177	312
ð	Query Match	43.5	40.7	40.3	0	39.1		7	37.5	37.1	7	37.1	7	7	7	9	36.7	9	•	•		36.3		ė.	ů.	ů.	•	'n.	'n,	
	Score	54		50				47		46						'n.	45.5	ū.				4.5					44.5	44		44
		П	CI	m	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	unknown protein en	conserved hypothet	hypothetical prote	unknown in ISEc8 [	choline dehydrogen	choline dehydrogen	choline dehydrogen	gramicidin S synth	gramicidin S synth	myosin heavy chain	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote
E91112	G85957	D87366	C90796	G85656	S10901	A85524	E90673	JX0340	YGBSG2	A27224	C72668	T27645	A90985	D85830	C64970
7	Ŋ	N	7	7	н	N	(7	N	-	-	N	N	N	N	N
467	467	512	537	537	556	562	562	4450	4452	1509	145	388	406	406	406
35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.1	34.7	34.7	34.7	34.7	34.7
44	44	44	44	44	44	44	44	44	44	43.5	43	43	43	43	43
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1	
	hypothetical protein APE0749 - Aeropyrum pernix (strain K1)	
	C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text_change 09-Jul-2004	11-2004
	C;Accession: F72665	
	R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.;	.; Jin-no, K.; Take
	awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;	Y.; Yamazaki, J.;
	DNA Res. 6, 83-101, 1999	
	A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy	renarchaeon, Aeropi
_	A;Reference number: A72450; MUID:99310339; PMID:10382966	
	A;Accession: F72665	
	A;Status: preliminary	
_	A; Molecule type: DNA	
	A;Residues: 1-187 <kaw></kaw>	
_	A;Cross-references: UNIPROT:Q9YE21; DDBJ:AP000060; NID:g5104188; PIDN:BAA79726.1; PID:	N:BAA79726.1; PID:
	A; Experimental source: strain Kl	
	C;Genetics:	
	A; Gene: APE0749	
	Query Match 43.5%; Score 54; DB 2; Length 187;	
	Best Local Similarity 57.9%; Pred. No. 0.91;	
	Matches 11; Conservative 1; Mismatches 7; Indels 0; Ga	Gaps 0;
	Qy 4 YKPIADLYRGRESRPSAPR 22	
	Db 35 YKLVGLLYLGRELRPKLPR 53	

CiSpecies: Symechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr.1997 #sequence\_revision 25-Apr.1997 #text\_change 09-Jul-2004
C;Date: 25-Apr.1997 #sequence\_revision 25-Apr.1997 #text\_change 09-Jul-2004
C;Accession: 874629
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
C; Wigowura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuc
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocyst: hypothetical protein sll1686 - Synechocystis sp. (strain PCC 6803)

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74629
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-488 cKAN>
A;Cross-references: UNIPROT:P72766; EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAA16'
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Ξ, Gaps ۲; Length 488; 4; Indels Query Match
Best Local Similarity 44.4%; Pred. No. 8.6;
Matches 8; Conservative 5; Mismatches 4; ä

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A,Title: Structure of a gene in the dipteran Chironomus tentans encoding a yeast riboson A,Reference number: S26380, MUID:93065218; PMID:1437565
A,Accession: S26380
A,Accession: S26380
A,Restaus: nucleic acid sequence not shown
A,Rolecule type: mRNA
A,Residues: 1-204 <GAL>
A,Residues: 1-204 <GAL>
CSOSAURE: 1-204 <GAL>
CSOSAURE: 1-204 <GAL>
CSOSAURE: Tibosomal protein L15
C;Keywords: protein blosynthesis; ribosome
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A;Cross-references: EMBL:U53343; NID:g1255881; PID:g1255883; PIDN:AAA96220.1; GSPDB:GNO
A;Experimental source: strain Bristol N2; clone F22F4
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C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehyd
C;Keywords: oxidoreductase
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A;Title: Isolation, DNA sequence analysis, and mutagenesis of a proline dehydrogenase A;Reference number: Z21008; MUID:96141420; PMID:8572700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C;Accession: I16141
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Cispecies: Bradyrhizobium japonicum
Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
CiAccession: T31343
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Pred. No. 64;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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A,Molecule type: DNA
A,Residues: 1-1016 <STR>
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A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Pred. No. 18;
2; Mismatches
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Pred. No. 6.8;
3; Mismatches
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Best Local Similarity 45.5%;
Matches 10; Conservative
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Best Local Similarity 47.8%;
Matches 11; Conservative
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A,Introns: 8/2; 59/2; 386/3
C,Superfamily: Passover protein
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Best Local Similarity 50.08
Matches 9; Conservative
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Discovery (C; Maccossion: A84806
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Usayam, L.; Tallon, L. Wizture 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accossion: A84806
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C.Species: Arabidopsis thaliana (mouse-ear ress)
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
R.Abordence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Reference number: A85001; MUID:20083488; PMID:10617198
A.Reference number: A85006
A.Reference number: A85006
A.Reference number: A85006
A.Reference number: A85006
A.Reference number: A85006
A.Reference number: A85001
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N;Alternate names: ribosomal protein YL10 homolog
C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S26380; 285633
R;Accession: J; Wieslander, L.
Nucleic Acids Res. 20, 5473, 1992
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4.3;
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Pred. No. 5.7;
3; Mismatches 3
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130 PWQYRPVS-IQLGRRPKP 146
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                                                                       1 PWQYKPIADLYRGRESRP 18
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188 EPIADLFRKKRERPS 202
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
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